

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 1, 2005, 09:34:17 ; Search time 114 Seconds
(without alignments)
588.442 Million cell updates/sec

Title: US-10-617-876-1

Perfect score: 668

Sequence: 1 MANKMPQITSTANKIWSDD.....NAGLGFLDPTAAIVSSDTTA 131

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt 03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	668	100.0	131	2	Q9AZ42
2	80	12.0	194	1	LPPK MYCLE
3	79	11.8	918	1	IL6B HUMAN
4	78.5	11.8	559	2	Q26645
5	78.5	11.8	667	2	Q6LOE7
6	78	11.7	305	2	Q9RT24
7	78	11.7	6146	2	Q93HJ5
8	77.5	11.6	1454	2	Q8ENZ2
9	77	11.5	373	2	Q74KV6
10	77	11.5	1088	2	Q6ZUM6
11	76.5	11.5	457	2	Q6CJF9
12	76.5	11.5	546	1	CH60_CHRVI
13	76	11.4	436	2	Q74BT9
14	76	11.4	538	2	Q7WS88
15	76	11.4	540	2	Q7SG34
16	75.5	11.3	519	1	ACHG_BOVIN
17	75.5	11.3	1174	2	Q8MPR0
18	75	11.2	386	2	Q8P9T4
19	75	11.2	711	2	Q6MKR4
20	74.5	11.2	1333	2	Q6L3N8
21	74	11.1	620	2	Q12623
22	74	11.1	657	1	GTK_CHICK
23	74	11.1	713	2	Q8EV63
24	74	11.1	988	2	Q87ID1
25	74	11.1	1693	2	Q7RLG9
26	74	11.1	2799	1	G112_HUMAN
27	73.5	11.0	213	2	O50402
28	73.5	11.0	291	2	Q9SBF9
29	73.5	11.0	236	2	Q7TWL6
30	73.5	11.0	830	2	Q9U3V0
31	73.5	11.0	831	2	Q92D26

32	73.5	11.0	3550	2	Q66GT4	Q66gt4 rattus norv
33	73.5	11.0	7048	2	Q6D739	Q6d739 erwinia car
34	73	10.9	214	2	Q9SXH1	Q9sxh1 physcomitre
35	73	10.9	547	2	Q8Y5Y8	Q8y5y8 listeria mo
36	72	10.8	273	1	FWDC_METJA	O58571 methanococc
37	72	10.8	517	2	Q8FBE3	Q8fbb3 escherichia
38	72	10.8	524	2	Q42147	Q42147 xenopus lae
39	72	10.8	524	2	Q8AVN9	Q8avn9 xenopus lae
40	72	10.8	680	2	Q9N9G7	Q9n9g7 phallusia m
41	72	10.8	1084	2	Q6BGK7	Q6bgk7 paramecium
42	72	10.8	4032	2	Q7WTF3	Q7wtf3 streptomyce
43	71.5	10.7	173	2	Q9AI69	Q9aig9 helicobacte
44	71.5	10.7	619	2	Q8H8S5	Q8h8s5 oryza sativ
45	71.5	10.7	1199	1	TTL4_HUMAN	Q14679 homo sapien

ALIGNMENTS

RESULT 1

Q9AZ42 PRELIMINARY; PRT; 131 AA.
AC Q9AZ42;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Coat protein.
OS Bacteriophage AP205.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
OC Levivirus.
OX NCBI_TaxID=154784;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22024855; PubMed=12029168;
RA Klovins J., Overbeek G.P., van den Worm S.H., Ackermann H.W.,
RA van Duin J.,
RT "Nucleotide sequence of a ssRNA phage from Acinetobacter: kinship to
RT coliphages.";
RL J. Gen. Virol. 83:1523-1533(2002).
RN [2]
RP SEQUENCE FROM N.A.
RA Klovins J.,
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF334111; AAK20390.1; -;
DR GO; GO:0019028; C:Viral capsid; IEA.
DR GO; GO:0005198; P:Structural molecule activity; IEA.
KW Coat protein.
SQ SEQUENCE 131 AA; 14009 MW; FB4ECBCEB8E12982 CRC64;

Query Match 100.0%; Score 668; DB 2; Length 131;
Best Local Similarity 100.0%; Pred. No. 8.1e-60;
Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MANKMPQITSTANKIWSDDPTRLSTTFSASLLRQVKVGIARLNNSGQVSVYKRPAP 60

DB 1 MANKMPQITSTANKIWSDDPTRLSTTFSASLLRQVKVGIARLNNSGQVSVYKRPAP 60

QY 61 KPEGCADACVIMPNENQSIPTVSSAENLATLKAEWETHKRNVDTLFASGNAGLGFLDP 120

DB 61 KPEGCADACVIMPNENQSIPTVSSAENLATLKAEWETHKRNVDTLFASGNAGLGFLDP 120

QY 121 TAAIVSSDTTA 131

DB 121 TAAIVSSDTTA 131

RESULT 2

LPPK MYCLE STANDARD; PRT; 194 AA.
ID LPPK MYCLE
AC Q49803;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)

DE Putative lipoprotein lppK precursor.
GN Name=lppK; OrderedLocName=ML1315;
GN ORFNames=MLCB2533.llc, B2126_F3_115;
OS Mycobacterium leprae.
OC Bacteria; Actinobacteria; Actinobacteriales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1769;
RN [1]
RP SEQUENCE FROM N.A.
RA Smith D.R., Robison K.;
RL Submitted (MAR-1994) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=TN;
RX MEDLINE=21128732; PubMed=11234002; DOI=10.1038/35059006;
RA Cole S.T., Eiglmeyer K., Parkhill J., James K.D., Thomson N.R.,
RA Wheeler P.R., Honore N., Garnier T., Churchev C.M., Harris D.E.,
RA Mungall K.L., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N.,
RA Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,
RA Murphy L.D., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,
RA Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,
RA Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
RA Barrall B.G.;
RL "Massive gene decay in the leprosy bacillus";
RL Nature 409:1007-1011(2001).
CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor (Potential).
CC -1- SIMILARITY: Belongs to the MTB12 family.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
CC EMBL; U00017; AAA17217.1; --
DR EMBL; AL035310; CAA22925.1; --
DR EMBL; AL583921; CAC31696.1; --
DR PIR; S72877; S72877.
DR Leproma; ML1315; --
DR InterPro; IPR000437; Prok lipoprot_S
DR PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
KW Complete proteome; Hypothetical protein; Lipoprotein; Membrane;
KW Palmitate; Signal.
FT SIGNAL 1 26 Potential.
FT CHAIN 27 194 Putative lipoprotein lppK.
FT LIPID 27 27 S-diacylglycerol cysteine (By similarity).
FT LIPID 27 27 N-palmitoyl cysteine (By similarity).
SQ SEQUENCE 194 AA; 20460 MW; E575262FC3218A86 CRC64;
Query Match 12.0%; Score 80; DB 1; Length 194;
Best Local Similarity 25.0%; Pred No. 6.4;
Matches 30; Conservative 10; Mismatches 26; Indels 54; Gaps 6;
Qy 8 PITSTANKIYMS--DPTSLSTFTSASLLRQVKVGIAGLNNVSGQYVSVKY-----RPAP 60
Db 110 PMTFTANNIAWSNKNPSDVLATIS-----VNIAQTNN-----SVFSFPMFTFPF 154
Qy 61 KPECCADACVIMPENOSIRTVISGSANLATLKAETHKRVVDITLPSAGNAGLGFDP 120
Db 155 PPQ-----QSWLSKRTADMLLEFGNSG-GLTNP 182
RESULT 3
IL6B_HUMAN
ID IL6B_HUMAN STANDARD; PRT; 918 AA.
AC P40189; Q9UQ41;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)

DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Interleukin-6 receptor beta chain precursor (IL-6R-beta) (Interleukin
DE 6 signal transducer) (Membrane glycoprotein 130) (gp130) (Oncostatin M
DE receptor) (CDW130) (CD130 antigen).
GN Name=IL6ST;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX TISSUE=Myeloma, and Placenta;
RX MEDLINE=91084844; PubMed=2261637; DOI=10.1016/0092-8674(90)90411-7;
RA Hibi M., Murakami M., Saito M., Hirano T., Taga T., Kishimoto T.;
RT "Molecular cloning and expression of an IL-6 signal transducer,
RT gp130";
RL Cell 63:1149-1157(1990).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RX TISSUE=Synovium;
RX MEDLINE=20341529; PubMed=10880057;
RA Tanaka M., Kishimura M., Ozaki S., Osakada F., Hashimoto H., Okubo M.,
RA Murakami M., Nakao K.;
RT "Cloning of novel soluble gp130 and detection of its neutralizing
RT autoantibodies in rheumatoid arthritis";
RL J. Clin. Invest. 106:137-144(2000).
RN [3]
RP PARTIAL SEQUENCE, DISULFIDE BONDS, AND CARBOHYDRATE-LINKAGE SITES.
RX MEDLINE=21269388; PubMed=11098061; DOI=10.1074/jbc.M009979200;
RA Moritz R.L., Hall N.E., Connolly L.M., Simpson R.J.;
RT "Determination of the disulfide structure and N-glycosylation sites of
RT the extracellular domain of the human signal transducer gp130";
RL J. Biol. Chem. 276:8244-8253(2001).
RN [4]
RP "Crystal structure of a cytokine-binding region of gp130";
RX Bravo J., Staunton D., Heath J.K., Jones E.Y.;
RT "Crystal structure of a cytokine-binding region of gp130";
RL EMBL J. 17:1665-1674(1998).
CC -1- FUNCTION: Signal-transducing molecule. The receptor systems for
CC IL6, LIF, OSM, CNTF, IL11 and CT1 can utilize gp130 for initiating
CC signal transduction. Binds to IL6/IL6R (alpha chain) complex,
CC resulting in the formation of high-affinity IL6 binding sites, and
CC transduces the signal. Does not bind IL6. May have a role in
CC embryonic development (By similarity).
CC -1- SUBUNIT: Heterodimer of an alpha and a beta chain.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (isoform 1).
CC Secreted (isoform 2).
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=P40189-1; Sequence=Displayed;
CC Name=2; Synonyms=GP130-RAPS;
CC IsoId=P40189-2; Sequence=VSP_001684, VSP_001685;
CC -1- TISSUE SPECIFICITY: Found in all the tissues and cell lines
CC examined. Expression not restricted to IL-6 responsive cells.
CC -1- DOMAIN: The WSXWS motif appears to be necessary for proper protein
CC folding and thereby efficient intracellular transport and cell-
CC surface receptor binding.
CC -1- DOMAIN: The box 1 motif is required for JAK interaction and/or
CC activation.
CC -1- DISEASE: Isoform 2 is an autoantigen found in rheumatoid arthritis
CC (RA) but it is not specific to patients with RA.
CC -1- SIMILARITY: Belongs to the type I cytokine family of receptors.
CC Subfamily 2.
CC -1- SIMILARITY: Contains 5 fibronectin type III domains.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
CC -1- DATABASE: NAME=PROW; NOTE=CD guide CD130 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd130.htm"
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its


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DR GO: GO:0005634; C:nucleus; IEA.
DR GO: GO:0003700; F:transcription factor activity; IEA.
DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro: IPR000418; Ets.
DR InterPro: IPR002341; HSF.ETS.
DR InterPro: IPR010993; SAM_homology.
DR InterPro: IPR003118; SAM_PNT.
DR Pfam: PF001178; Ets; 1.
DR Pfam: PF02198; SAM_PNT; 1.
DR PRINTS: PR00454; ETSDOMAIN.
DR SMART: SM00413; ETS; 1.
DR SMART: SM00251; SAM_PNT; 1.
DR PROSITE: PS00345; ETS_DOMAIN_1; 1.
DR PROSITE: PS00346; ETS_DOMAIN_2; 1.
DR PROSITE: PS0061; ETS_DOMAIN_3; 1.
KW DNA-binding; Nuclear protein.
SQ SEQUENCE 559 AA; 62052 MW; 509EAFCT7ACBD21 CRC64;

Query Match 11.8%; Score 78.5; DB 2; Length 559;
Best Local Similarity 25.5%; Pred. No. 33;
Matches 40; Conservative 27; Mismatches 51; Indels 39; Gaps 7;

QY 2 ANKPMQ---PITSTANKIVWSDP-----TRLSTTFGASLLRQVRKVGIAELNNVSGQYVS 53
DB 208 ANVPAOSSSTSTSSSSSTASPPVSVTTTITTTTASSSSLSQIK-----LENVSSGYLN 262
QY 54 V-----YKRP-----APKEGCADACVIMPENQSIQRTVIVSSAENLA 91
DB 263 TTSCMPLDLFLAQGSVDQPAQVSPAPQCSFSDG---MYQVESLQITNEFNADIL 319
QY 92 TLKAEWETHKRNVDTLFASGNAGIGFLD-PTAAIVSS 127
DB 320 NIKQEDTGSDDYVLESSPNSQHFLETPTEIYNN 356

RESULT 5
Q6LQ67 PRELIMINARY; PRT; 667 AA.
AC Q6LQ67
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical methyl-accepting chemotaxis protein.
GN Names:PSPT0323; OrderedLocusNames:PBPA2077;
OS Photobacterium profundum (Photobacterium sp. (strain SS9)).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Photobacterium.
OX NCBI_TaxID=74109;
RN [1]
RP SEQUENCE FROM N.A.
RA Vezzi A., Campanaro S., D'Angelo M., Simonato F., Vitulo N., Lauro F.,
RA Cestaro A., Malacrida G., Simonati B., Camata N., Bartlett D.,
RA Valle G.;
RT "Genome analysis of Photobacterium profundum reveals the complexity of
RT high pressure adaptations.";
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: CR378669; CAC20479.1; -.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0004871; F:signal transducer activity; IEA.
DR GO: GO:0006935; P:chemotaxis; IEA.
DR GO: GO:0007165; P:signal transduction; IEA.
DR InterPro: IPR004089; Chmtaxis trans.
DR InterPro: IPR003660; His_kin_HAMP.
DR Pfam: PF00672; T_SNARE.
DR SMART: SM00283; MA; 1.
DR PROSITE: PS0111; CHEMOTAXIS_TRANSDUC_2; 1.
DR PROSITE: PS00885; HAMP; 1.
DR PROSITE: PS0192; T_SNARE; 1.
KW Complete proteome; Hypothetical protein.
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```
SQ SEQUENCE 667 AA; 73612 MW; B1D05DE9D060532C CRC64;

Query Match 11.8%; Score 78.5; DB 2; Length 667;
Best Local Similarity 24.8%; Pred. No. 41;
Matches 35; Conservative 22; Mismatches 53; Indels 31; Gaps 6;

QY 2 ANKPMQPIIT-----STANKIVWSDPTRLSTTFGASLLRQVRKVGIAELNNVSGQYVS 55
DB 420 ANETMQVITAINEMASTABEVARTNTTTSNTHNATVAADQSK---AAVNKATDSVALLM 476
QY 56 KRPAKPEGCADACVIMPENQSIQRTVIS-----GSAENLATLKAWEETHKRNVDTLFAS 110
DB 477 TQIETASENTE-----MSNETQKISITVLNVIRIDIAEQTNLLALNAIEAAR-----A 524
QY 111 GNAGLGLDPTAAIVSSDTTA 131
DB 525 GDQGRGF-----AVVADEVRA 540

RESULT 6
Q9RT24 PRELIMINARY; PRT; 305 AA.
AC Q9RT24
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Malonyl CoA-acyl carrier protein transacylase.
GN OrderedLocusNames:DR11945;
OS Deinococcus radiodurans.
OC Bacteria; Deinococcus-Thermus; Deinococci; Deinococcales;
OC Deinococcaceae; Deinococcus.
OX NCBI_TaxID=1299;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RI / ATCC 13939 / DSM 20539 / NCIB 9279;
RX MEDLINE=20036896; PubMed=10567266; DOI=10.1126/science.286.5444.1571;
RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
RA Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
RA Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
RA Vamathevan J.J., Lam P., McDonald L.A., Uitterback T.R., Zalewski C.,
RA Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
RA Ketchum K.A., Nelson K.E., Salzberg S.L., Smith H.O., Venter J.C.,
RA Fraser C.M.;
RT "Genome sequence of the radioresistant bacterium Deinococcus
RT radiodurans R1.";
RL Science 286:1571-1577(1999).
DR EMBL: AE002033; AAF11497.1; -.
DR PIR: A75334; A75334.
DR HSSP: P25715; IMLA.
DR TIGR: DR1945; -.
DR GO: GO:0016740; F:transferase activity; IEA.
DR GO: GO:0004314; F:[acyl-carrier protein] S-malonyltransferase. .; IEA.
DR GO: GO:0006833; P:fatty acid biosynthesis; IEA.
DR GO: GO:0008152; P:metabolism; IEA.
DR InterPro: IPR001227; Ac transferase.
DR InterPro: IPR004410; Fabb.
DR Pfam: PF00698; Acyl transf 1; 1.
DR TIGRFAMs: TIGR00128; fabd; 1.
DR Complete proteome.
KW SEQUENCE 305 AA; 31284 MW; 0564188B9FA35B9F CRC64;

Query Match 11.7%; Score 78; DB 2; Length 305;
Best Local Similarity 28.9%; Pred. No. 18;
Matches 35; Conservative 14; Mismatches 62; Indels 10; Gaps 4;

QY 13 ANKIVWSDPTRLSTTFGASLLRQVRKVGIAELNNVSGQYVSVKRPAPKEGC-ADACVI 71
DB 103 AGVLTLEDALRL--TRKRGELMQQAVPEGVGMSAVMGD-----PAVVAEVCQAQGVV 154
QY 72 MP-NENQSIQRTVISGSAENLATLKAWEETHKRNVDTLFASGNAGLGLDPTAAIVSSDTT 130
DB 155 QPANFNAPTQTVISGEKAAVDAAASAEIKTKGLKAIPLKVSAPFCALMRPAEGLSAELH 214
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QY 131 A 131
 Db 215 A 215
 RESULT 7
 Q93HJ5 PRELIMINARY; PRT; 6146 AA.
 ID Q93HJ5
 AC Q93HJ5
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Modular polyketide synthase.
 GN Namesolmal; OrderedLocusNames=SAV2899;
 OS Streptomyces avermitilis.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Streptomycineae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=33903;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MA-4680;
 RX MEDLINE=21477403; PubMed=11572948; DOI=10.1073/pnas.211433198;
 RA Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,
 RA Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osone T.,
 RA Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
 RT "Genome sequence of an industrial microorganism Streptomyces
 RT avermitilis: deducing the ability of producing secondary
 RT metabolites."
 RL Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MA-4680;
 RX MEDLINE=22608306; PubMed=12692562;
 RA Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T.,
 RA Sakaki Y., Hattori M., Omura S.;
 RT "Complete genome sequence and comparative analysis of the industrial
 RT microorganism Streptomyces avermitilis."
 RL Nat. Biotechnol. 21:526-531(2003).
 DR ENBL; AB070940; BAB69192.1;
 DR ENBL; AP005033; BAC70610.1;
 DR HSP; P6202; IPW.
 DR GO; GO:0004024; F:alcohol dehydrogenase activity, zinc-dependent; IEA.
 DR GO; GO:0048037; F:cofactor binding; IEA.
 DR GO; GO:0003960; F:NADPH:quinone reductase activity; IEA.
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0008270; F:zinc ion binding; IEA.
 DR GO; GO:0006333; F:fatty acid biosynthesis; IEA.
 DR GO; GO:0008152; F:metabolism; IEA.
 DR InterPro; IPR009081; ACP like.
 DR InterPro; IPR001227; Ac transferase.
 DR InterPro; IPR002198; ADH short.
 DR InterPro; IPR002085; Adh_zn_family.
 DR InterPro; IPR000794; ketoacyl synth.
 DR InterPro; IPR000209; Pept S8 S53.
 DR InterPro; IPR006163; Phosphateth_bind.
 DR InterPro; IPR006162; Phantne S.
 DR InterPro; IPR002364; OOR zeta_crystal.
 DR Pfam; PF00698; Acyl_transf_1; 4.
 DR Pfam; PF00106; adh_short; 1.
 DR Pfam; PF00107; ADH_zinc_N; 1.
 DR Pfam; PF00109; ketoacyl-synth; 4.
 DR Pfam; PF02801; ketoacyl-synt C; 4.
 DR Pfam; PF00550; PP-binding; 4.
 DR PROSITE; PS00075; ACP_DOMAIN; 4.
 DR PROSITE; PS00606; B_KETOACYL_SYNTHASE; 3.
 DR PROSITE; PS00012; PHOSPHOPANTETHEINE; 3.
 DR PROSITE; PS01162; OOR ZETA CRYSTAL; 1.
 DR PROSITE; PS01136; SUBTILASE ASP; UNKNOWN 1.
 KW Complete proteome; Phosphopantetheine; Transferrase.
 SQ SEQUENCE 6146 AA; 637476 MW; 1D56F1108D459D00 CRC64;
 Query Match 11.7%; Score 78; DB 2; Length 6146;
 Best Local Similarity 36.1%; Pred. No. 7.2e+02;
 Matches 35; Conservative 10; Mismatches 42; Indels 10; Gaps 4;
 QY 24 LSTFTSASLLRQVKVIGIAELNNVSGQYVYKRPAPKEGCA---DACVIMPENQSI 79
 Db 3100 LSLEDGAALVTLRSRL-IARELSGHGVMVSVALSPADTAERIARWNGGICVAANNSRRS- 3157
 QY 80 RTVISGSAENLATLKAWE---THKRVNVTLPASGNA 113
 Db 3158 -TVSGEPEALAEACEAEGVRARRIPVDYASHSA 3193
 RESULT 8
 Q8ENZ2 PRELIMINARY; PRT; 1454 AA.
 ID Q8ENZ2
 AC Q8ENZ2;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Bacillopeptidase F (EC 3.4.21.-).
 GN OrderedLocusNames=OB2331;
 OS Oceanobacillus iheyensis.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Oceanobacillus.
 OX NCBI_TaxID=182710;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=HTE831;
 RX MEDLINE=22220767; PubMed=12235376; DOI=10.1093/nar/gkf526;
 RA Takami H., Takaki Y., Uchiyama I.;
 RT "Genome sequence of Oceanobacillus iheyensis isolated from the Iheya
 RT ridge and its unexpected adaptive capabilities to extreme
 RT environments."
 RL Nucleic Acids Res. 30:3927-3935(2002).
 CC -I- SIMILARITY: Belongs to peptidase family S8.
 DR ENBL; AP004600; BAC14287.1;
 DR HSP; Q9405; IMPT.
 DR MEROPS; S08.017; -.
 DR GO; GO:0008233; F:peptidase activity; IEA.
 DR GO; GO:0004289; F:subtilase activity; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR000209; Pept S8 S53.
 DR InterPro; IPR009020; Prot_inh_propept.
 DR InterPro; IPR010259; Prot_inh_S8a.
 DR Pfam; PF00082; Peptidase S8; 1.
 DR Pfam; PF05922; Subtilisin N; 1.
 DR PRINTS; PR00723; SUBTILISIN.
 DR PROSITE; PS00137; SUBTILASE HIS; 1.
 DR PROSITE; PS00138; SUBTILASE_SER; 1.
 KW Complete proteome; Hydrolase; Protease; Serine protease.
 SQ SEQUENCE 1454 AA; 155494 MW; 9223ADF205D7FF7F CRC64;
 Query Match 11.6%; Score 77.5; DB 2; Length 1454;
 Best Local Similarity 29.4%; Pred. No. 1.4e+02;
 Matches 25; Conservative 15; Mismatches 42; Indels 3; Gaps 1;
 QY 47 VSGQYVYKRPAPKEGCAACVIMPENQSI RTVISGSAENLATLKAWE THKRVNVT 106
 Db 165 VNGIATVATKVAEKVATFAEVEKILPNETRELYTTVDKDAE---TPKSDVANVENVER 221
 QY 107 LPASGNAGLGLDPTAAIVSSDTTA 131
 Db 222 VGAPATWNNMGFDGSGVVVASIDTGA 246
 RESULT 9
 Q74KV6 PRELIMINARY; PRT; 373 AA.
 ID Q74KV6
 AC Q74KV6;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE DNA polymerase IV.
 GN OrderedLocusNames=LJ0471;
 Query Match 11.7%; Score 78; DB 2; Length 6146;

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OS Lactobacillus johnsonii.
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC Lactobacillus.
OX NCBI_TaxID=33959;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NCC 533;
RX PubMed=14966310;
RA Pittet A.-C., Zwahlen M.-C., Rouvet M., Altermann E., Barrangou R.,
RA Mollet B., Mercenier A., Klaenhammer T., Arigoni F., Schell M.A.;
RA "The genome sequence of the probiotic intestinal bacterium
RT Lactobacillus johnsonii NCC 533."
RL Proc. Natl. Acad. Sci. U.S.A. 101:2512-2517(2004).
DR EMBL; AE017201; AAS08463.1; -.
DR GO; GO:0006281; P:DNA repair; IEA.
DR Pfam; PF00817; IMS; 1.
DR PROSITE; PS01073; UMOU; 1.
KW Complete proteome.
SQ SEQUENCE 373 AA; 42240 MW; 3D2A1421FD195BE7 CRC64;

Query Match 11.5%; Score 77; DB 2; Length 373;
Best Local Similarity 27.6%; Pred. No. 29;
Matches 21; Conservative 14; Mismatches 25; Indels 16; Gaps 3;

QY 12 TANKIVMSDPRLSTSTFSAILLRV--KVGIAE-----LNNVSGYVSVYKRPAP 60
DB 124 TENKLNITDPVRI-----ALLQRIYQRIGLTSSFGVSNKFLAKMGSEYAKPFGRTVI 178
QY 61 KPEGACADACVMPNEN 76
DB 179 KPEGARDFLAKQPIKN 194

RESULT 10
Q6ZUM6 PRELIMINARY; PRT; 1088 AA.
AC Q6ZUM6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein FLJ43536.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA Kawakami B., Sugiyama A., Takemoto M., Sugiyama T., Irie R.,
RA Osuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,
RA Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,
RA Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M.,
RA Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A., Suzuki Y.,
RA Sugano S., Nagahori K., Masuko Y., Nagai K., Isogai T.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK125224; BAC86194.1; -.
FT NON TER 1088
SQ SEQUENCE 1088 AA; 126002 MW; A08B75393ADC564A CRC64;

Query Match 11.5%; Score 77; DB 2; Length 1088;
Best Local Similarity 29.7%; Pred. No. 1.1e+02;
Matches 15; Conservative 15; Mismatches 14; Indels 16; Gaps 3;

QY 41 IAEILNNVSGYVSVYKRPAPKPEGACADACVMP-----NENQSIPTVSGSAENLATLK 94
DB 963 VEEIGDANLQYSKIQER---KPE-----ILLPLFQEAEDKNLLRTVAGGLETISNLK 1012
QY 95 AEWE 98
DB 1013 AKWD 1016

RESULT 11
Q6C3F9 PRELIMINARY; PRT; 457 AA.
AC Q6C3F9;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE Similar to sp|P08540 Klyveromyces lactis Potential acid
DE phosphatase.
GN CRPNames=YALI0E35222g;
OS Yarrowia lipolytica CLIB99.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Dipodascaceae; Yarrowia.
OX NCBI_TaxID=284591;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CLIB99;
RG Genolevures;
RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,
RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
RA Barney S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
RA Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
RA Hantraye F., Hennequin C., Jaumiaux N., Joyet P., Kachouri R.,
RA Kerrest A., Kozul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA Nicaud J.M., Nikolski M., Ostas S., Ozier-Kalogeropoulos O.,
RA Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
RA Swennene D., Tekala S., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
RA Wincker P., Souciet J.L.;
RT "Genome evolution in yeasts.";
RL Nature 430:35-44(2004).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CLIB99;
RA Genoscope;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR382131; CAG80411.1; -.
DR GO; GO:0016788; F:Hydrolase activity, acting on ester bonds; IEA.
DR InterPro; IPR007312; Pesterase.
DR Pfam; PF04185; Phosphoesterase; 1.
SQ SEQUENCE 457 AA; 50001 MW; 523BE4A48FB34C4C CRC64;

Query Match 11.5%; Score 76.5; DB 2; Length 457;
Best Local Similarity 23.7%; Pred. No. 41;
Matches 32; Conservative 20; Mismatches 34; Indels 49; Gaps 6;

QY 46 NVSGQVSVYKRP-APKPEGACADACVIMP-NENQ-----SIRTVISGA----- 87
DB 242 SVSGRVTVNWVPLNNTFANDSLIITFDENETTKQNSVLAILLGGAVPDHLRGTTD 301
QY 88 -----ENLATLKAWE-----THKRNVDY--LPASGNAGLG 116
DB 302 DTFYDHYSNLATVEANWELPHLGRGDVNAVVKFVADENIKRNISTEGLYHNASQPGY 361
QY 117 FLDPTAAIVSSDTTA 131
DB 362 FMDDTVPIVPPDLTA 376

RESULT 12
CH60_CHRVI STANDARD; PRT; 546 AA.
ID CH60_CHRVI
AC P31293;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE 60 kDa chaperonin (Protein Cpn60) (groEL protein).
GN Name=groL; Synonyms=groEL, mopA;
OS Chromatium vinosum.

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SQ SEQUENCE 540 AA; 60340 MW; BCAB82CBE127046F CRC64;

Query Match      11.4%; Score 76; DB 2; Length 540;
Best Local Similarity 23.6%; Pred. No. 57;
Matches 34; Conservative 19; Mismatches 57; Indels 34; Gaps 5;

Qy   5 PMOPISTANKI VWSBPTRLSTTFSA-SILLRQKVKGI-AELNVSGQYVSV----- 55
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db   27 PKOPL-----FSDVSHLLTHCSKSHLSHRPKTEIPARHNDARETTQQVLKWEES 78
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

Qy   56 -----KRPAP--KPEGADACVIMPENOSIRTVISGSANLTLTKAEWE 98
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db   79 GIHALLEDLEAKENKKPAKRGPAGTANRPKAFQNRDDLVKNEAQEQLDHTPVLAWHI 138
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

Qy   99 THKRNVDTLFASGNAGIGFLDPTA 122
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db   139 TDPNNA SFQHNLRHGHSYLDPPA 162
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

Search completed: June 1, 2005, 09:45:53
Job time : 117 secs
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BT, 05-JUL-2004 (TREMBLER). 27, Last annotation update,

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DE Hypothetical methyl-accepting chemotaxis protein.
GN Names=PSPTO323; OrderedLocNames=PPRA2077;
OS Photobacterium profundum (Photobacterium sp. (strain SS9)).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Photobacterium.
OX NCBI_TaxID=74109;
RN [1]
RP SEQUENCE FROM N.A.
RA Vezzi A., Campanaro S., D'Angelo M., Simonato F., Vitulo N., Lauro F.,
RA Cestaro A., Malacrida G., Simonati B., Cannata N., Bartlett D.,
RA Valle G.;
RT "Genome analysis of Photobacterium profundum reveals the complexity of
RT high pressure adaptations."
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR ENBL; CR378669; CAC20479.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0006935; P:chemotaxis; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR004089; Chmtaxis transd.
DR InterPro; IPR003660; His kin HAMP.
DR InterPro; IPR000727; T-SNARE-.
DR Pfam; PF00672; HAMP; 1.
DR Pfam; PF00015; MCPsignal; 1.
DR SMART; SM00304; HAMP; 1.
DR SMART; SM00283; MA; 1.
DR PROSITE; PS0111; CHEMOTAXIS_TRANSLOC_2; 1.
DR PROSITE; PS0885; HAMP; 1.
DR PROSITE; PS0192; T-SNARE; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 667 AA; 73612 MW; B1D05DE90D60532C CRC64;

Query Match 12.78; Score 84.5; DB 2; Length 667;
Best Local Similarity 25.5%; Pred. No. 10; Mismatches 52; Indels 31; Gaps 6;
Matches 36; Conservative 22;

QY 2 ANKTMQPIIT-----STANKIVMSDPTRLSTTSASLLRQVKVIGIAELNNVSGQYVSVY 55
DB 420 ANETMQVITAINEMASTAEVARTTNTVNTHTNATVAADQSK---AAVNKATDSVALLM 476

QY 56 KRPAKPEGCADACVIMPNENQSIPTVIS-----GSAENLATLKAETHKRVNVDITLFA 110
DB 477 TQIETASENVT-----MSNETQKISTVLNVIRDAEQTNLLALMAATEAAR-----A 524

QY 111 GNAGLGLDPTAIVSSDTTA 131
DB 525 GDQGRGF-----AVVADEVRA 540

RESULT 3
LPPK_MYCLE
ID LPPK_MYCLE STANDARD; PRT; 194 AA.
AC Q49803;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Putative lipoprotein lppK precursor.
GN Name=lppK; OrderedLocNames=ML1315;
GN ORFNames=MLCB2533.lnc, B2126_F3_l15;
OS Mycobacterium leprae.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1769;
RN [1]
RP SEQUENCE FROM N.A.
RA Smith D.R., Robison K.;
RL Submitted (MAR-1994) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=TW;
RX MEDLINE=21128732; PubMed=11234002; DOI=10.1038/35059006;
RA Cole S.T., Biglmeier K., Parkhill J., James K.D., Thomson N.R.,
RA Wheeler P.R., Honore N., Garnier T., Churcher C.M., Harris D.E.,

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RA Mungall K.L., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N.,
RA Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,
RA Murphy L.D., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,
RA Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,
RA Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
RA Barrell B.G.;
RT "Massive gene decay in the leprosy bacillus."
RL Nature 409:1007-1011(2001).
CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor
CC (Potential).
CC -1- SIMILARITY: Belongs to the MTB12 family.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC -----
CC ENBL; U00017; AA17217.1; -.
CC DR ENBL; AL035310; CAA22925.1; -.
CC DR ENBL; AL583921; CAC31696.1; -.
CC DR PIR; S72877; S72877.
CC DR Leproma; ML1315; -.
CC DR InterPro; IPR000437; Prok lipoprot S.
CC DR PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
KW Complete proteome; Hypothetical protein; Lipoprotein; Membrane;
KW Palmitate; Signal.
FT SIGNAL 1 26 Potential.
FT CHAIN 27 194 Putative lipoprotein lppK.
FT LIPID 27 27 S-diacylglycerol cysteine (By
FT LIPID 27 27 similarity).
FT LIPID 27 27 N-palmitoyl cysteine (By similarity).
SQ SEQUENCE 194 AA; 20460 MW; E975262FC3218A86 CRC84;

Query Match 12.0%; Score 80; DB 1; Length 194;
Best Local Similarity 25.0%; Pred. No. 6.5; Mismatches 26; Indels 54; Gaps 6;
Matches 30; Conservative 10;

QY 8 PITSTANKIVMS--DPTRLSTTSASLLRQVKVIGIAELNNVSGQYVSVYK-----RPAP 60
DB 110 PMTFTANNIAWSKNPDSVLATIS-----VNIAQTNN-----SVSPFMEFTFPF 154

QY 61 KPESGCADACVIMPNENQSIPTVISGSAENLATLKAETHKRVNVDITLFA 120
DB 155 PPO-----QSWQLSKRTADMLLEFGNS-GLTNP 182

RESULT 4
IL6B_HUMAN
ID IL6B_HUMAN STANDARD; PRT; 918 AA.
AC P40189; Q9U041;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Interleukin-6 receptor beta chain precursor (IL-6R-beta) (Interleukin
DE 6 signal transducer) (Membrane glycoprotein 130) (gp130) (Oncostatin M
DE receptor) (CDw130) (CD130 antigen).
GN Name=IL6ST;
GN Homo sapiens (Human).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Myeloma, and Placenta;
RX MEDLINE=91084844; PubMed=2261637; DOI=10.1016/0092-8674(90)90411-7;
RA Hibi M., Murakami M., Saito M., Hirano T., Taga T., Kishimoto T.;
RT "Molecular cloning and expression of an IL-6 signal transducer,
RT gp130."
RL Cell 63:1149-1157(1990).

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RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RC TISSUE=Synovium;
 RX MEDLINE=20341529; PubMed=10880057;
 RA Tanaka M., Kishimura M., Ozaki S., Osakada F., Hashimoto H., Okubo M.,
 RT Murakami M., Nakao K.;
 RT "cloning of novel soluble gp130 and detection of its neutralizing
 RT autoantibodies in rheumatoid arthritis";
 RL J. Clin. Invest. 106:137-144 (2000).
 RN [3]
 RP PARTIAL SEQUENCE, DISULFIDE BONDS, AND CARBOHYDRATE-LINKAGE SITES.
 RX MEDLINE=21269388; PubMed=11098061; DOI=10.1074/jbc.M009979200;
 RA Moritz R.L., Hall N.E., Connolly L.M., Simpson R.J.;
 RT "determination of the disulfide structure and N-glycosylation sites of
 RT the extracellular domain of the human signal transducer gp130.";
 RL J. Biol. Chem. 276:8244-8253 (2001).
 RN [4]
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 122-325.
 RX MEDLINE=98169383; PubMed=9501088; DOI=10.1093/embioj/17.6.1665;
 RA Bravo J., Staunton D., Heath J.K., Jones E.Y.;
 RT "Crystal structure of a cytokine-binding region of gp130.";
 RL EMBO J. 17:1665-1674 (1998).
 CC -I- FUNCTION: Signal-transducing molecule. The receptor systems for
 CC IL6, LIF, OSM, CNTF, IL11 and CT1 can utilize gp130 for initiating
 CC signal transduction. Binds to IL6/IL6R (alpha chain) complex,
 CC resulting in the formation of high-affinity IL6 binding sites, and
 CC transduces the signal. Does not bind IL6. May have a role in
 CC embryonic development (By similarity).
 CC -I- SUBUNIT: Heterodimer of an alpha and a beta chain.
 CC -I- SUBCELLULAR LOCATION: Type I membrane protein (isoform 1).
 CC Secreted (isoform 2).
 CC -I- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=P40189-1; Sequence=Displayed;
 CC Name=2; Synonyms=GP130-RAPS;
 CC IsoId=P40189-2; Sequence=VSP_001684, VSP_001685;
 CC -I- TISSUE SPECIFICITY: Found in all the tissues and cell lines
 CC examined. Expression not restricted to IL-6 responsive cells.
 CC -I- DOMAIN: The WSXWS motif appears to be necessary for proper protein
 CC folding and thereby efficient intracellular transport and cell-
 CC surface receptor binding.
 CC -I- DOMAIN: The box 1 motif is required for JAK interaction and/or
 CC activation.
 CC -I- DISEASE: Isoform 2 is an autoantigen found in rheumatoid arthritis
 CC (RA) but it is not specific to patients with RA.
 CC -I- SIMILARITY: Belongs to the type I cytokine family of receptors.
 CC Subfamily 2.
 CC -I- SIMILARITY: Contains 5 fibronectin type III domains.
 CC -I- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
 CC -I- DATABASE: NAME=PROW; NOTE=CD guide CD130 entry;
 CC WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd130.htm".
 CC -----
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 CC -----
 CC EMBL; M57230; AAA59155.1; --
 CC EMBL; AB015706; BAA78112.1; --
 CC PIR; A36337; A36337.
 CC PDB; 1BJ8; NMR; @=217-325.
 CC PDB; 1BQJ; X-ray; A/B=119-333.
 CC PDB; 1IIR; X-ray; A=23-325.
 CC Genew; HGNC:6021; IL6ST.
 CC MIM; 600594; --
 CC GO; GO:0005887; C:integral to plasma membrane; TAS.
 CC GO; GO:0004915; F:interleukin-6 receptor activity; TAS.
 CC GO; GO:0004924; F:oncostatin-M receptor activity; TAS.
 CC GO; GO:0004872; F:receptor activity; TAS.

DR GO; GO:0007166; P:cell surface receptor linked signal transdu. .; TAS.
 DR InterPro; IPR002996; Cytokn_recept_B/G.
 DR InterPro; IPR003961; FN_III.
 DR InterPro; IPR008957; FN_III-like.
 DR InterPro; IPR003529; Hemtrecept_1302.
 DR InterPro; IPR010457; Lep_receptor_Ig.
 DR Pfam; PF00041; fn3; 3.
 DR PROSITE; PS06328; Lep_receptor_Ig; 1.
 DR PROSITE; PS0853; FN3; 5.
 KW PROSITE; PS01353; HEMATOPO_REC_L_F2; 1.
 KW 3D-structure; Alternative splicing; Direct protein sequencing;
 KW Glycoprotein; Immunoglobulin domain; Receptor; Repeat; Signal;
 KW Transmembrane.
 FT SIGNAL 1 22 Interleukin-6 receptor beta chain.
 FT CHAIN 23 918 Extracellular (Potential).
 FT DOMAIN 23 619 Potential.
 FT TRANSMEM 620 641 Cytoplasmic (Potential).
 FT DOMAIN 642 918 Ig-like C2-type.
 FT DOMAIN 26 120 Fibronectin type-III 1.
 FT DOMAIN 125 216 Fibronectin type-III 2.
 FT DOMAIN 222 321 Fibronectin type-III 3.
 FT DOMAIN 326 418 Fibronectin type-III 4.
 FT DOMAIN 423 514 Fibronectin type-III 5.
 FT DOMAIN 518 610 Ser-rich.
 FT DOMAIN 725 755 WSXWS motif.
 FT SITE 310 314 Box 1 motif.
 FT SITE 651 659
 FT DISULFID 28 54
 FT DISULFID 48 103
 FT DISULFID 134 144
 FT DISULFID 172 182
 FT DISULFID 458 466
 FT CARBOHYD 43 43 N-linked (GlcNAc...)
 FT CARBOHYD 83 83 N-linked (GlcNAc...)
 FT CARBOHYD 131 131 N-linked (GlcNAc...)
 FT CARBOHYD 157 157 N-linked (GlcNAc...)
 FT CARBOHYD 227 227 N-linked (GlcNAc...)
 FT CARBOHYD 379 379 N-linked (GlcNAc...)
 FT CARBOHYD 383 383 N-linked (GlcNAc...)
 FT CARBOHYD 553 553 N-linked (GlcNAc...)
 FT CARBOHYD 564 564 N-linked (GlcNAc...)
 FT VARSPLIC 325 329 RPSKA -> NIASF (in isoform 2).
 FT FTID=VSP_001684.
 FT Missing (in isoform 2).
 FT VARSPLIC 330 918 /FTID=VSP_001685.
 FT STRAND 29 32
 FT STRAND 37 39
 FT TURN 40 41
 FT STRAND 44 50
 FT HELIX 52 58
 FT TURN 59 59
 FT TURN 62 64
 FT STRAND 65 69
 FT TURN 70 71
 FT STRAND 72 73
 FT STRAND 76 78
 FT HELIX 80 83
 FT TURN 84 85
 FT STRAND 86 91
 FT STRAND 98 107
 FT TURN 108 110
 FT STRAND 111 123
 FT STRAND 130 137
 FT TURN 138 139
 FT STRAND 143 147
 FT STRAND 157 164
 FT TURN 165 166
 FT TURN 165 168
 FT STRAND 172 173
 FT TURN 179 180
 FT STRAND 181 183
 FT TURN 190 191

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FT STRAND 194 202
FT TURN 203 204
FT STRAND 205 208
FT STRAND 212 214
FT HELIX 216 219
FT STRAND 220 221
FT STRAND 226 231
FT STRAND 240 245
FT STRAND 248 251
FT HELIX 252 252
FT STRAND 255 263
FT TURN 264 265
FT STRAND 270 271
FT HELIX 274 277
FT STRAND 283 286
FT TURN 291 292
FT STRAND 294 303
FT TURN 304 305
FT STRAND 317 320
SQ SEQUENCE 918 AA; 103522 MW; D813F3672DD10D53 CRC64;

Query Match 11.9%; Score 79; DB 1; Length 918;
Best Local Similarity 25.5%; Pred. No. 55;
Matches 25; Conservative 21; Mismatches 36; Indels 16; Gaps 5;

QY 9 ITSTANKIVMSDPTRLSTTPFSASILLR-QRVKVGIAELNNVSGQVSVYKRPAPKPGCAD 67
DB 82 INTASSVTFDTASLNQICNTLTFGQLEQNVYGIISG-----LPPEKPNL-- 132

QY 68 ACVIMPENOSIRTVISGSAENLA----TLKAEWETHK 101
DB 133 SCIV--NEGKMKRCWDGGRETHLETNFTLKSEWATHK 168

RESULT 5
Q9RT24 PRELIMINARY; PRT; 305 AA.
AC Q9RT24;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE Malonyl CoA-acyl carrier protein (transacylase)
GN OrderedLocusNames=DR1945;
OS Deinococcus radiodurans.
OC Bacteria; Deinococcus-Thermus; Deinococci; Deinococcales;
OC Deinococcaceae; Deinococcus.
OX NCBI_TaxID=1299;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=R1 / ATCC 13939 / DSM 20539 / NCIB 9279;
RX MEDLINE=20036896; PubMed=10567266; DOI=10.1126/science.286.5444.1571;
RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
RA Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
RA Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
RA Vamathevan J.J., Lam P., McDonald L.A., Utterback T.R., Zalewski C.,
RA Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
RA Ketchum K.A., Nelson K.E., Salzberg S.L., Smith H.O., Venter J.C.,
RA Fraser C.M.;
RT "Genome sequence of the radioresistant bacterium Deinococcus
RT radiodurans R1";
RL Science 286:1571-1577(1999).
DR EMBL; AE002033; AAF11497.1; -.
DR PIR; A75334; A75334.
DR HSP; P25715; IMLA.
DR TIGR; DR1945; -.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0004314; F:acyl-carrier protein[S-malonyl]transferase. .; IEA.
DR GO; GO:0006633; P:fatty acid biosynthesis; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR001227; Ac:transferase.
DR InterPro; IPR004410; FAbD.
DR Pfam; PF00698; Acyl transf 1; 1.
DR TIGRFAMS; TIGR00126; fabD; 1.
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KW Complete proteome.
SQ SEQUENCE 305 AA; 31284 MW; 0564188B9FA35E9F CRC64;

Query Match 11.7%; Score 78; DB 2; Length 305;
Best Local Similarity 28.9%; Pred. No. 18;
Matches 35; Conservative 14; Mismatches 62; Indels 10; Gaps 4;

QY 13 ANKIVMSDPTRLSTTPFSASILLRQVRKVGIAELNNVSGQVSVYKRPAPKPGC-ADACVI 71
DB 103 AGVITLEDALRL-TRKRGELMQAVPEGVGMASVWGD-----PAAVVEVCAAGVV 154

QY 72 MP-NENOSIRTVISGSAENLATLKAETHKRNVDTLFASGNAGLGLDPTAAIVSSDTT 130
DB 155 QPANFNAPTQTVISGEKAAVDAASAEKTRGLKAIPKVSAPPHCALMRPAEGLSAELH 214

QY 131 A 131
DB 215 A 215

RESULT 6
Q42147 PRELIMINARY; PRT; 524 AA.
ID Q42147;
AC Q42147;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE DarBP-Zfa.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97415754; PubMed=9268652; DOI=10.1006/jmbi.1997.1177;
RA Finerty P.J., Jr., Bass B.L.;
RT "A Xenopus zinc finger protein that specifically binds dsRNA and RNA-
RT DNA hybrids.";
RL J. Mol. Biol. 271:195-208(1997).
DR EMBL; AF005083; AAC60260.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR InterPro; IPR000345; CytC_heme_BS.
DR InterPro; IPR007087; Znf_C2H2.
DR InterPro; IPR003604; Znf_U1.
DR SMART; SM00355; Znf_C2H2; 7.
DR SMART; SM00451; Znf_U1; 7.
DR PROSITE; PS00190; CYTOCHROME C; UNKNOWN 1.
DR PROSITE; PS00028; ZINC FINGER_C2H2_1; UNKNOWN 7.
SQ SEQUENCE 524 AA; 55588 MW; 104D6603ADB8D57 CRC64;

Query Match 11.7%; Score 78; DB 2; Length 524;
Best Local Similarity 26.9%; Pred. No. 35;
Matches 42; Conservative 20; Mismatches 62; Indels 32; Gaps 8;

QY 2 ANKTMQPISTTA--NKIVMSDPTRL-----STPFSASLL-----RQVRKVGIAEL 44
DB 139 AKKTRTPTVATKSDNKMDSHSDRAKFCCLKHSTFNNPLMAEQHVAGKHKHKQETKTQIMTI 198

QY 45 NNVSQGVSVYKRP----APKP-EGCA-----DACVIMPENOSIRTVISGSAEN---L 90
DB 199 YTSGGQTTPAQAPIPLNLNFMFGSGSGAGKGFCDKCNIVLNSIEQYCAHVSGAKHKQLM 258

QY 91 ATLKAETHKRNVDTLFASGNAGLGLDPTAAIV 125
DB 259 SMTPLSEEGHQAQVAPSAIASGAGKGFCDTCNIV 294

RESULT 7
Q8AVN9 PRELIMINARY; PRT; 524 AA.
ID Q8AVN9
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Best Local Similarity 36.1%, Pred. No. 7.2e+02;
Matches 35; Conservative 10; Mismatches 42; Indels 10; Gaps 4;

QY 24 LSTTFSSASLRLQKRVGIAELNNVSGYVYKRPAPKPEGCA----DACVIMPENQSI 79
DB 3100 LSLDGAALVTLASRL-IAELSCHGGVSVASPADTAERLARWNGGICVAANSRRS- 3157

QY 80 RTVVISGSAENLATLKAWE---THKRNVDTLFASGNA 113
DB 3158 -TVVSGPEALAECEAEGVRARRIPVDYASHA 3193

RESULT 9
Q8MPEO Q8MPEO PRELIMINARY; PRT; 1174 AA.
AC Q8MPEO;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DE Bone morphogenetic protein type 2 receptor.
GN Name=BMP-R2 gene;
OS Crassostrea gigas (Pacific oyster).
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Ostreoida;
OC Ostreoida; Ostreidae; Crassostrea.
OX NCBI_TaxID=29159;
RN [1]
RP SEQUENCE FROM N.A.
RA Herpin A.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ427420; CAD20574.1; -.
DR HSSP; P36897; I1AS.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004672; F:protein kinase activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0005024; F:transforming growth factor beta receptor ac. .; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR GO; GO:0007178; P:transmembrane receptor protein serine/threo. .; IEA.
DR InterPro; IPR00472; Actinin receptor.
DR InterPro; IPR000333; Actn_receptorII.
DR InterPro; IPR011009; Kinase-like.
DR InterPro; IPR000719; Prot_kinase.
DR PRINTS; PR00653; ACTVIN2R.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW Receptor.
SQ SEQUENCE 1174 AA; 132154 MW; 5E3928BD1406507A CRC64;

Query Match 11.6%; Score 77.5; DB 2; Length 1174;
Best Local Similarity 26.9%; Pred. No. 1.1e+02;
Matches 36; Conservative 23; Mismatches 48; Indels 27; Gaps 8;

QY 5 TMQPIITANKI-VWSDPTRLSTFSSASLRLQKRVGIAE-----LNNVSGQYV---- 52
DB 686 TTTPTITTSNFSQISSPETHPTTA-MAPTEETGADTNSTASVMVINSPPNGYITSRP 744
QY 53 -SVYKRPAPKEG-CADACVIM-PENQSI---IRTVISGSAENLATLK-----AEWE 98
DB 745 SSWNRCMTSGTSTFTTFVMSPEDEAPPVKLLNNLAKNNTVLPVHQGRIPIAERN 804
QY 99 THKRNVDTLFASGNA 112
DB 805 THKRSDELSVSGN 818

RESULT 10
Q8ENZ2 Q8ENZ2 PRELIMINARY; PRT; 1454 AA.
AC Q8ENZ2;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DE Bacillopeptidase F (EC 3.4.21.-).
GN OrderedLocusNames=OB2331;

OS Oceanobacillus iheyensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Oceanobacillus.
OX NCBI_TaxID=182710;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HTE831;
RX MEDLINE=22220767; PubMed=12235376; DOI=10.1093/nar/gkf526;
RA Takami H., Takaki Y., Uchiyama I.;
RT "Genome sequence of Oceanobacillus iheyensis isolated from the Iheya Ridge and its unexpected adaptive capabilities to extreme environments."
RT Nucleic Acids Res. 30:3927-3935 (2002).
CC -I- SIMILARITY: Belongs to peptidase family S8.
DR EMBL; AF004600; BAC14287.1; -.
DR HSSP; Q99405; LMPT.
DR MEROPS; S08.017; -.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004289; F:subtilase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR000209; Pept_S8_S53.
DR InterPro; IPR009020; Prot_inh_S8A.
DR InterPro; IPR010259; Prot_inh_S8A.
DR Pfam; PF00082; Peptidase_S8; 1.
DR Pfam; PF05922; Subtilisin_N; 1.
DR PRINTS; PR00723; SUBTILISIN.
DR PROSITE; PS00137; SUBTILASE_HIS; 1.
DR PROSITE; PS00138; SUBTILASE_SER; 1.
KW Complete proteome; Hydrolase; Protease; Serine protease.
SQ SEQUENCE 1454 AA; 155494 MW; 9223ADF205D7FF7F CRC64;

Query Match 11.6%; Score 77.5; DB 2; Length 1454;
Best Local Similarity 29.4%; Pred. No. 1.4e+02;
Matches 25; Conservative 15; Mismatches 42; Indels 3; Gaps 1;

QY 47 VSCQYVSVYKRPAPKEGCAACVIMPENQSI---IRTVISGSAENLATLKAWEHTRKNDT 106
DB 165 VNGIATVATKKAQVATTAEEVEKILNETRELYTTVDKDAE---TPKSDVANVEMNVER 221
QY 107 LFASGNAGLGLDPTAAIVSSDTTA 131
DB 222 VGAPATWNGFGDSGVVASIDTGA 246

RESULT 11
Q74KV6 Q74KV6 PRELIMINARY; PRT; 373 AA.
AC Q74KV6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE DNA polymerase IV.
GN OrderedLocusNames=LJ0471;
OS Lactobacillus johnsonii.
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC Lactobacillus.
OX NCBI_TaxID=33959;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NCC 533;
RX PubMed=14966310;
RA Pridmore R.D., Rouvet M., Altermann E., Barrangou R.,
RA Pittet A.-C., Zwahlen M.-C., Klaenhammer T., Arigoni F., Schell M.A.;
RA Mollet B., Mercenier A., Klaenhammer T., Arigoni F., Schell M.A.;
RT "The genome sequence of the probiotic intestinal bacterium Lactobacillus johnsonii NCC 533."
RT Proc. Natl. Acad. Sci. U.S.A. 101:2512-2517 (2004).
DR EMBL; AE017201; AAS08463.1; -.
DR GO; GO:0006281; P:DNA repair; IEA.
DR InterPro; IPR001126; UMUC_like.
DR Pfam; PF00817; IMS; 1.
DR PROSITE; PS50173; UMUC; 1.
KW Complete proteome.
SQ SEQUENCE 373 AA; 42240 MW; 3D2A1421FD195BE7 CRC64;
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Query Match 11.6%; Score 77; DB 2; Length 373;
Best Local Similarity 27.6%; Pred. No. 29;
Matches 21; Conservative 14; Mismatches 25; Indels 16; Gaps 3;

QY 12 TANKVMSDPTSTSTFASILLRQV--KVGIAE-----LNNVSGYVSVYKRPAP 60
Db 124 TENKLNITDPRI-----ALLQRIYQRIGLTSSFGVSYNKFAMGSEYAKPFGRTVI 178
QY 61 KPGECADACVMPNEN 76
Db 179 KPEGARDFLAKQPIKN 194

RESULT 12
Q6ZUM6 Q6ZUM6 PRELIMINARY; PRT; 1088 AA.
AC Q6ZUM6;
DT 05-JUL-2004 (T-EMBLrel. 27, Created)
DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
DE Hypothetical protein FLJ43536.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA Kawakami B., Sugiyama A., Takemoto M., Sugiyama T., Irie R.,
RA Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,
RA Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,
RA Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M.,
RA Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A., Suzuki Y.,
RA Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AKI2524; BAC86194.1; -
FT NON TER 1088
SQ SEQUENCE 1088 AA; 126002 MW; A08B75393ADC564A CRC64;

Query Match 11.6%; Score 77; DB 2; Length 1088;
Best Local Similarity 29.7%; Pred. No. 11e+02;
Matches 19; Conservative 15; Mismatches 14; Indels 16; Gaps 3;

QY 41 IAEIANNVSGYVSVYKRPAPKPGCADACVIMP-----NENOSIRTVISGSAENLATLK 94
Db 963 VERIGDANLQYSKLOER--KPE-----ILPLFQEAEDKRLRTVAGGLETISNLK 1012
QY 95 AEWE 98
Db 1013 AKWD 1016

RESULT 13
Q6C3F9 Q6C3F9 PRELIMINARY; PRT; 457 AA.
AC Q6C3F9;
DT 25-OCT-2004 (T-EMBLrel. 28, Created)
DT 25-OCT-2004 (T-EMBLrel. 28, Last sequence update)
DE Similar to sp|P08540 Kluyveromyces fragilis Potential acid
DE phosphatase.
GN ORFName=YALI0E35222g;
OS Yarrowia lipolytica CLIB99.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Dipodascaceae; Yarrowia.
OX NCBI_TaxID=284591;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CLIB99;
RG Genolevures;
RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,
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RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
RA Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
RA Boisrame A., Boyer J., Cattolico L., Confanioli F., de Daruvar A.,
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi R.,
RA Hantaye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA Niclaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
RA Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
RA Swemene D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
RA Wincker P., Souciet J.L.;
RT "Genome evolution in yeasts.";
RL Nature 430:35-44(2004).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CLIB99;
RA Genoscope; (JUL-2004) to the EMBL/GenBank/DBJ databases.
RL Submitted (JUL-2004); CAG80411.1; -
DR EMBL; CR382131; CAG80411.1; -
DR GO; GO:0016788; F-hydrolase activity, acting on ester bonds; IEA.
DR InterPro; IPR007312; Pesterase.
DR Pfam; PF04185; Phosphoesterase; 1.
SQ SEQUENCE 457 AA; 50001 MW; 523BE4A48PB34C4C CRC64;

Query Match 11.5%; Score 76.5; DB 2; Length 457;
Best Local Similarity 23.7%; Pred. No. 42;
Matches 32; Conservative 20; Mismatches 34; Indels 49; Gaps 6;

QY 46 NVSGQVSVYKRP-APKPGCADACVIMP-NENQ-----SIRTVISGSA----- 87
Db 242 SVSGRYVTWVKKPLNLTTEFAKDSLIITFDENETYKQNSVLAILLGAVPDLRGTTD 301
QY 88 -----ENLATLKAWE-----THKRNVDI--LFASGNAGLG 116
Db 302 DFYDHYSNLATVEANWELPHLGRGDVNAVFKFVADENIKRNISTEGLYNNASQPGY 361
QY 117 FLDPTAAIVSSDTTA 131
Db 362 FMDTVPVPDLTA 376

RESULT 14
CH60_CHRVI CH60_CHRVI STANDARD; PRT; 546 AA.
AC P31233;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE 60 kDa chaperonin (Protein Cpn60) (groEL protein).
GN Name=grol; Synonyms=groEL, mopA;
OS Chromatium vinosum.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Chromatiales;
OC Chromatiaceae; Allochromatium.
OX NCBI_TaxID=1049;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93186721; PubMed=8444812;
RA Ferreyra R., Soncini F., Viale A.M.;
RT "Cloning, characterization, and functional expression in Escherichia
RT coli of chaperonin (groEL) genes from the phototrophic sulfur
RT bacterium Chromatium vinosum.";
RL J. Bacteriol. 175:1514-1523(1993).
RN [2]
RP CHARACTERIZATION.
RX MEDLINE=99008942; PubMed=9790891; DOI=10.1006/prep.1998.0953;
RA Dionisi H.M., Viale A.M.;
RT "Purification and characterization of Chromatium vinosum GroEL and
RT GroES proteins overexpressed in Escherichia coli cells lacking the
RT endogenous groEL operon.";
RL Protein Expr. Purif. 14:275-282(1998).
CC -I- FUNCTION: Prevents misfolding and promotes the refolding and
CC proper assembly of unfolded polypeptides generated under stress
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CC conditions.
CC -1- SUBUNIT: Oligomer of 14 subunits composed of two stacked rings of
CC 7 subunits.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: Belongs to the chaperonin (HSP60) family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@ebi.ac.uk).
CC -----
CC EMBL: M99443; AAA23319.1; -.
CC PIR: B47073; B47073.
CC HSP; P06139; IGR5.
CC HAMAP; MF 00600; -.
CC InterPro; IPR001844; Chaperonin Cpn60.
CC InterPro; IPR002423; Cpn60/TCP-1.
CC InterPro; IPR008950; GroEL-ATPase.
CC Pfam; PF00118; Cpn60_TCP1; 1.
CC PRINTS; PR00298; CHAPERONIN60.
CC PRINTS; PR00304; TCOMPLEXTCF1.
CC PROSITE; PS00296; CHAPERONIN_CPN60; 1.
CC ATP-binding; Chaperone.
CC SEQUENCE 546 AA; 57541 MW; 3250141881C04DD6 CRC64;
Query Match 11.5%; Score 76.5; DB 1; Length 546;
Best Local Similarity 20.7%; Pred. No. 52;
Matches 28; Conservative 25; Mismatches 65; Indels 17; Gaps 3;
QY 3 NKTQPTITANKI--VMSDPTLSTTFSASLLRQVRKVGIAELN-----NVS 48
Db 68 NMGAQMKVKEVASKTSDTAGDGTATVLAQAMVREGKVAAGNPNMCLKRMKMDKAVEAA 127
QY 49 GQYVSVYKRPAPKEGCADACVIMPENQISRTVVISGAENL---ATLKAWEETHKRNVD 105
Db 128 TEELKLSKCPRPMAAQVGTISANSDDSGIHTIAEMKEVKGIVTVDGTSIQNEL 187
QY 106 TLFASGNAGLGFDDP 120
Db 188 DVVEGMOFDRGYLSP 202
RESULT 15
Q871D1 Q871D1 PRELIMINARY; PRT; 988 AA.
AC Q871D1;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Sensor protein TorS.
GN OrderedLocuNames=VPA0675;
OS Vibrio parahaemolyticus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=670;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RIMD 2210633 / Serotype O3:K6;
RX MEDLINE=22508454; PubMed=12620739; DOI=10.1016/S0140-6736(03)12659-1;
RA Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,
RA Iijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,
RA Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;
RT "Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism
RT distinct from that of V. cholerae.";
RL Lancet 361:743-749(2003).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -1- SIMILARITY: Contains 1 histidine kinase domain.
DR EMBL; AP005086; BAC62018.1; -.
DR HSP; Q9A514; 1MAV.
DR GO; GO:0016021; C:integral to membrane; IEA.
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DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0016301; F:kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0000156; F:two-component response regulator activity; IEA.
DR GO; GO:0000155; F:two-component sensor molecule activity; IEA.
DR GO; GO:0007600; P:sensory perception; IEA.
DR GO; GO:0000160; P:two-component signal transduction system (p...); IEA.
DR InterPro; IPR003594; ATPbind ATPase.
DR InterPro; IPR004358; Bact_sens_pr_C.
DR InterPro; IPR011006; Chev_like.
DR InterPro; IPR005467; His_kinase.
DR InterPro; IPR003661; His_kin N.
DR InterPro; IPR003660; His_kin HAM.
DR InterPro; IPR009082; His_kin_homodim.
DR InterPro; IPR008207; Hpt.
DR InterPro; IPR001789; Response_reg.
DR Pfam; PF00672; HAM; 1.
DR Pfam; PF02518; HATPase_C; 1.
DR Pfam; PF00512; HsKa; 1.
DR Pfam; PF01627; Hpt; 1.
DR Pfam; PF00072; Response_reg; 1.
DR PRINTS; PR00344; BCTRLSENSOR.
DR PRODOM; PD000039; Response_reg; 1.
DR SMART; SM00304; HAM; 1.
DR SMART; SM00387; HATPase_C; 1.
DR SMART; SM00388; HsKa; 1.
DR SMART; SM00073; HPT; 1.
DR SMART; SM00448; REC; 1.
DR PROSITE; PS00885; HAM; 1.
DR PROSITE; PS0109; HIS_KIN; 1.
DR PROSITE; PS0894; HPT; 1.
DR PROSITE; PS0110; RESPONSE_REGULATORY; 1.
KW Complete proteome; Kinase; Phosphorylation; Sensory transduction;
KW Transference; Transmembrane.
SQ SEQUENCE 988 AA; 109882 MW; 962F67DF6A44BC72 CRC64;
Query Match 11.5%; Score 76.5; DB 2; Length 988;
Best Local Similarity 24.7%; Pred. No. 11e+02;
Matches 36; Conservative 18; Mismatches 47; Indels 45; Gaps 6;
QY 1 MANKTQW---PITSTANKIVMSDPTLSTTFSASLLRQVRKVGIAELNNVS----- 48
Db 295 LMQKTLFLFSELNSTVKNLV--DDSNKTTTFAVDQLTNTLKFAQWSLTVISGLIVVVL 352
QY 49 ----GQYVSVYKRPAP-----KPE--GCADACVIMPENQSIRT 81
Db 353 ILWRVYVYVVKRLAAYSALLSVAQGNLALEVKGKDELAHMQQAIIITARTAQAKV 412
QY 82 VISGSAENLATLKAWEETHKRNVDTL 107
Db 413 VAEGEAK----AKRELEEHKEHLEEL 434
Search completed: June 1, 2005, 09:45:54
Job time : 115 secs
```

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	80	12.0	194	2	S72877	hypothetical prote
2	79	11.9	918	2	A53337	membrane glycoprot
3	78	11.7	305	2	A75334	lacyl-carrier-prot
4	76.5	11.5	546	2	B47073	chaperonin GroEL -
5	75.5	11.3	519	2	I45847	acetylcholine rece
6	73.5	11.0	213	2	D70972	probable enoyl-coA
7	73.5	11.0	291	2	T51668	myb-related trans
8	73.5	11.0	831	2	A11515	ORF of Listeria s
9	73	11.0	547	2	AC3314	malolactic enzyme
10	72	10.8	273	2	B64446	formylmethanofuran
11	71.5	10.7	220	2	T14951	hypothetical prote
12	71.5	10.7	942	1	J01674	protein kinase TMK
13	71	10.7	562	2	S38149	SIS2 protein - yea
14	70.5	10.6	414	2	A80229	hypothetical prote
15	70.5	10.6	536	2	JG0022	flagellar basal-bo
16	70	10.5	519	2	I56566	nicotinic acetylch
17	70	10.5	519	2	S13874	nicotinic acetylch
18	69.5	10.4	358	2	T27862	hypothetical prote
19	69.5	10.4	358	2	S31407	(2'-5')oligo(A) sy
20	69.5	10.4	643	2	I50539	intermediate filam
21	69.5	10.4	26926	1	I38344	titin, cardiac mus
22	69	10.4	374	2	T10415	virus envelope pro
23	69	10.4	666	2	S29349	hypothetical prote
24	69	10.4	2187	2	S60224	polyketide synthas
25	68	10.2	352	2	C69172	conserved hypothet
26	68	10.2	287	2	A97762	hypothetical prote
27	68	10.2	350	2	S51494	arabinogalactan en
28	68	10.2	454	2	I16522	mitosis-specific c
29	67.5	10.1	330	2	T37854	probable IUNH-fam

F;134-316/Domain:

A;Map position: 5q11-5q11
C;Keywords: glycoprotein; membrane protein
F;134-316/Domain: cytokine receptor homology <CRS>

```

Query Match      11.9%; Score 79; DB 2; Length 918;
Best Local Similarity 25.5%; Pred. No. 9.3;
Matches 25; Conservative 21; Mismatches 36; Indels 16; Gaps 5;

Qy 9 ITSTANKIVMSDDTRLSSTFSASLLR-QRVKVGIAELNNVSGQVSVYKRPAPKEGCAD 67
Db 82 INRTASVVTTRDASLNQITCNILTFGQLEQNVYGIITISG-----LPPEKPKNL-- 132
      ||| : : ||| : : : : : : : : : : : : : : : : : : : : : : : :
Qy 68 ACVIMPNENOSIRTVISGSAENLA----TLKAEWETHK 101
Db 133 SCIV--NEGKKMRCWGDGGRHETHLETNFTLKSEWATHK 168
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 3
A75334
[acyl-carrier-protein] S-malonyltransferase (EC 2.3.1.39) DR1945 [similarity] - Deinococcus
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: A75334
R;White, O.; Eisen, J.A.; Heidelberg, J.P.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896; PMID:10567266
A;Accession: A75334
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-305 <WHI>
A;Cross-references: UNIPROT:Q9RT24; GB:AE002033; GB:AE000513; NID:g6459726; PIDN:AAF1149
A;Experimental source: strain R1
C;Genetics:
A;Gene: DR1945
A;Map position: 1
C;Superfamily: [acyl-carrier-protein] S-malonyltransferase; [acyl-carrier-protein] S-mal
C;Keywords: acyltransferase; coenzyme A
F;7-286/Domain: [acyl-carrier-protein] S-malonyltransferase homology <AMT>
F;93/Active site: Ser (covalent substrate-binding) #status predicted
F;198/Active site: His #status predicted

Query Match      11.7%; Score 78; DB 2; Length 305;
Best Local Similarity 28.9%; Pred. No. 3.1;
Matches 35; Conservative 14; Mismatches 62; Indels 10; Gaps 4;

Qy 13 ANKIVMSDDPTRLSTFSASLLRQVKVGIAELNNVSGQVSVYKRPAPKEGC-ADACVI 71
Db 103 AGVLTLEDAURL-TRKRGELMQQAPVPGVGAMSGMD-----PAVVAEVCAAQAGVV 154
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 72 MP-NNENOSIRTVISGSAENLATLKAETHKRNVDITLFASGNAGLGFDPPTAAIVSSDIT 130
Db 155 QPANFNAPTQTVISGEKAAVDASAEKLTGRLKAIPLKVSAPFHCALMRPAEGLSAELH 214
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 131 A 131
Db 215 A 215

RESULT 4
B47073
chaperonin GroEL - Chromatium vinosum
C;Species: Chromatium vinosum
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: B47073
R;Ferreyra, R.G.; Soncini, F.C.; Viale, A.M.
J. Bacteriol. 175, 1514-1523, 1993
A;Title: Cloning, characterization, and functional expression in Escherichia coli of cha
A;Reference number: A47073; MUID:93186721; PMID:8444812
A;Accession: B47073
A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-546 <FER>
A;Cross-references: UNIPROT:P31293; GB:M99443; NID:g1450007; PIDN:AAA23319.1; PID:g1450009

```

A;Note: sequence extracted from NCBI backbone (NCBIN:126968, NCBIP:126970)
C;Superfamily: chaperonin groEL
C;Keywords: molecular chaperone

Query Match 11.5%; Score 76.5; DB 2; Length 546;
Best Local Similarity 20.7%; Pred. No. 9;
Matches 28; Conservative 25; Mismatches 65; Indels 17; Gaps

Qy 3 NKTMQPITSTANKI--VMSDPTLSTTFSASLLRQRVKVGIAEIN-----NVSS
| | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 68 NMGAQMVKVEASKTSDIAGDGTTATVLAQAMVREGIKAVAGMNPMDLKRGMDKAAVEA
| | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Qy 49 GQYVSYYKPAPKEGCADACVIMPNENQSIRTVISGSAEHL---ATLKAETHETKRNVD
| | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 128 TEELKKLSKCPRPMAIAQVGTITSANSDDSIGTHIIAEKMKVKEGVITVEDGTSIQNEH
| | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Qy 106 TLFASGNAGLGFLDP 120
| | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 188 DVVEGMQFDRGYLSP 202
| | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

RESULT 5
I45847
acetylcholine receptor - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 15-Oct-1996 #sequence_revision 15
C;Accession: I45847
R.;Takai, T.; Noda, M.; Furutani, Y.; Takahashi, H.; Notake, M.; Shimizu, S.
Eur. J. Biochem. 143, 109-115, 1994
A;Title: Primary structure of gamma subunit precursor of calf-muscle acetylcholine receptor
A;Reference number: I45847; MUID:84285374; PMID:6547904
A;Accession: I45847
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-519 <YAK>
A;Cross-references: UNIPROT:P13536; GB:M28307; NID:g162601; PIDN:AAA30351
C;Genetics:
A;Gene: ACHR
C;Superfamily: acetylcholine receptor
C;Keywords: neurotransmitter receptor

Query Match 11.3%; Score 75.5; DB 2; Length 519;
Best Local Similarity 23.4%; Pred. No. 11;
Matches 37; Conservative 20; Mismatches 62; Indels 39; Gaps

Qy 2 ANKTMQPITSTANKIVMSDPTLSTTFSASLLRQRVKVGIA-----ELNNVSGO---
| | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 370 AHPLQNGSSGWPIAGEVALCLPRSELLFRQRQNLVRRALEKLEKGPESGQSPPE
| | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

Qy 52 VSVYKRPAPKEGCADACVIMPNENQSIRTVISGSAEHLATLKAETHETKRNVD-----
| | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 430 CGSLKQAAPAIPAQCVAECNLIAARHQTHFDGSGN-----KEWPLVGRVLDRVCFLA
| | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

Qy 106 --TLFASGNAGLGFL-----DFTAAIVSSD 128
| | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 482 MLSLFCVCTGATFILMAHYNRVPALPPFGDPSRYLPSSD 519
| | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

RESULT 6
D70972
probable enoyl-coA hydratase - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 16-Aug-2001
C;Accession: D70972
r.;Cole, S.T.; Broesch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris,
Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, M.;
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares,
Nature 393, 537-544, 1998
A;Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell,
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the co
A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: D70972
A;Status: preliminary; nucleic acid sequence not shown; translation not sh

A;Molecule type: DNA
A;Residues: 1-213 <COL>
A;Cross-references: UNIPROT:O50402; GB:AL009198; GB:AL123456; NID:g3242262; PIDN:CAA1575
A;Experimental source: strain H37RV
C;Genetics:
A;Gene: echA18
C;Superfamily: Naphthoate synthase

Query Match 11.0%; Score 73.5; DB 2; Length 213;
Best Local Similarity 27.6%; Pred. No. 5.8;
Matches 24; Conservative 14; Mismatches 42; Indels 7; Gaps 3;

QY 33 LRORVKVGIAGLNNVSGQYVSV---YKRPAPKPGACACVIMPNENQSIPTVIGSGAE 88
Db 1 MRRRAWTKMDASNPCCGGDIAEMCQMRQPPAEGVVDVRVALQRHNVALLTSLHPQAQ 60
QY 89 NLATLKAWEETHKRNVDTLFASGNAGL 115
Db 61 NALNL-ASWRLKELLDDL--AGESGL 84

RESULT 7
T51668
myb-related transcription factor MYB61 [imported] - Arabidopsis thaliana (fragment)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 09-Jul-2004
C;Accession: T51668
R;Kranz, H.D.; Denekamp, M.; Greco, R.; Jin, H.; Kranz, H.D.; Denekamp, M.; Greco, R.; J.
Plant J. 16, 263-275, 1998
A;Title: Towards functional characterisation of the members of the R2R3-MYB gene from A.
A;Reference number: Z14349; MUID:9839469; PMID:9839469
A;Accession: T51668
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-291 <RA>
A;Cross-references: UNIPROT:Q9SBP9; EMBL:AF062896; PIDN:AAC83618.1
A;Experimental source: cultivar Columbia
C;Genetics:
A;Gene: MYB61
A;Map position: I
C;Keywords: transcription factor

Query Match 11.0%; Score 73.5; DB 2; Length 291;
Best Local Similarity 21.9%; Pred. No. 8.5;
Matches 30; Conservative 21; Mismatches 67; Indels 19; Gaps 4;

QY 3 NKTMQPITSTANKIVWSDPTRLSTTFSASLLRQVRKVGIAGLNNVS-----QQY 51
Db 78 HKSPSSSSATNQDFLERPSDLSDYFGQKLNFNLSGLSVTTDSSLCSMIPPQSPFGNM 137

QY 52 V-SVYKRPAPKPGACACVIMPNENQSIPTVIGSGAENLATLKAWEETHKRNVDTLFAS 110
Db 138 VGSVLQTPV-----CVKPSLSLPHDNNSSPSISGDHVHKLAPNWEFQTNNNNTSNFF-- 190

QY 111 GNAGLGLDPTAAIVSS 127
Db 191 DNGGFSNPSNSTSS 207

RESULT 8
A11515
ORF of *Listeria seeligeri*, (LPXTG motif) homolog lin0665 [imported] - *Listeria innocua*
C;Species: *Listeria innocua*
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Accession: A11515
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker,
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A;Title: Comparative genomics of *Listeria* species.

A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AC1314
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-547 <GLA>
A;Cross-references: UNIPROT:Q9YSY8; GB:NC_003210; PIDN:CAC99993.1; PID:gl6411368; GSPDB:C
A;Experimental source: strain EGD-e
C;Genetics:
A;Gene: lmo1915
C;Superfamily: malate dehydrogenase (oxaloacetate-decarboxylating)

Query Match 11.0%; Score 73; DB 2; Length 547;
Best Local Similarity 25.0%; Pred. No. 20;
Matches 33; Conservative 21; Mismatches 56; Indels 22; Gaps 4;

QY 12 TANKIVWSDPTRLSTTFSASLLRQVRKVGIAGLNNVSGQYVYKRPAPK-----PEGC 65
Db 191 TNNETLLNDPLYLG-----NKRPLSESEDAFIASFVNVKVFPAKLLHWEDFGR 242

QY 66 ADACVIMPNENQSIPTV-----ISGS-----AENLATLKAWEETHKRNVDTLFASGNAGLGF 117
Db 243 ANASRLHNYRDKICTFNDIIOQTGMVVAVALTIQVSRIPLSEQKIIFPGAGTAGIGI 302

QY 118 LDPTAAIVSSDT 129
Db 303 ADLSAQLMRET 314

RESULT 10
B64446
formylmethanofuran dehydrogenase (EC 1.2.99.5) (tungsten) chain C - *Methanococcus jannaschii*
C;Species: *Methanococcus jannaschii*
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 16-Aug-2004

A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: A11515
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-831 <GLA>
A;Cross-references: UNIPROT:Q92D26; GB:AL592022; PIDN:CAC95897.1; PID:gl64113105; GSPDB:C
A;Experimental source: strain Clp11262
C;Genetics:
A;Gene: lin0665

Query Match 11.0%; Score 73.5; DB 2; Length 831;
Best Local Similarity 25.8%; Pred. No. 30;
Matches 34; Conservative 18; Mismatches 53; Indels 27; Gaps 7;

QY 8 PITSTAN-KIVWSDPTRLSTTFSASLLRQVRKVGIAGLNNVSGQ-----YVSVYKRPAP-- 60
Db 646 PLVSDMNDKVKGVPGDYEVTLNA-----VNEDGVAAEAKTFIVRLKSPAPII 694

QY 61 --KPEGCACACVIMPNENQSIPTVIGSGAENLATL-----KAWEETHKRNVDTLFASGNA 113
Db 695 TVDPEVSYDSAI--KNETELLKEVRAKTDNSAITSADAPDKVKWQTPGSGYTTVLNAVND 753

QY 114 GLGFLDPTAAIV 125
Db 754 GIP-ADPVTFFIV 764

RESULT 9
AC1314
malolactate enzyme (malate dehydrogenase) homolog lmo1915 [imported] - *Listeria monocytogenes*
C;Species: *Listeria monocytogenes*
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Accession: AC1314
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker,
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A;Title: Comparative genomics of *Listeria* species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AC1314
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-547 <GLA>
A;Cross-references: UNIPROT:Q9YSY8; GB:NC_003210; PIDN:CAC99993.1; PID:gl6411368; GSPDB:C
A;Experimental source: strain EGD-e
C;Genetics:
A;Gene: lmo1915
C;Superfamily: malate dehydrogenase (oxaloacetate-decarboxylating)

Query Match 11.0%; Score 73; DB 2; Length 547;
Best Local Similarity 25.0%; Pred. No. 20;
Matches 33; Conservative 21; Mismatches 56; Indels 22; Gaps 4;

QY 12 TANKIVWSDPTRLSTTFSASLLRQVRKVGIAGLNNVSGQYVYKRPAPK-----PEGC 65
Db 191 TNNETLLNDPLYLG-----NKRPLSESEDAFIASFVNVKVFPAKLLHWEDFGR 242

QY 66 ADACVIMPNENQSIPTV-----ISGS-----AENLATLKAWEETHKRNVDTLFASGNAGLGF 117
Db 243 ANASRLHNYRDKICTFNDIIOQTGMVVAVALTIQVSRIPLSEQKIIFPGAGTAGIGI 302

QY 118 LDPTAAIVSSDT 129
Db 303 ADLSAQLMRET 314

RESULT 10
B64446
formylmethanofuran dehydrogenase (EC 1.2.99.5) (tungsten) chain C - *Methanococcus jannaschii*
C;Species: *Methanococcus jannaschii*
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 16-Aug-2004

R;Chang, C.; Schaller, G.E.; Patterson, S.E.; Kwok, S.F.; Meyerowitz, E.M.; Blecker, A.L.
Plant Cell 4, 1263-1271, 1992

A>Title: The TWK1 gene from Arabidopsis codes for a protein with structural and biochemical properties similar to those of the mammalian Twikins.

A:Reference number: JQ1674; PMID:93076110; PMID:1332795

A:Accession: JQ1674

A:Molecule type: DNA

A:Residues: 1-942 <CHIA>

A:Cross-references: UNIPROT:P43298; GB:L00670; NID:g166887; PIDN:AAA32876.1; PID:g166888

C:Superfamily: protein kinase xaz1; leucine-rich alpha-2-glycoprotein repeat homology; pkinase

C:Keywords: ATP; autophosphorylation; glycoprotein; phosphotransferase; receptor; serine/threonine kinase

F:1-22/Domain: signal sequence #status_predicted <SIG>

F:23-942/Product: protein kinase TWK1 #status_predicted <MAT>

F:65-88/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR1>

F:89-111/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR2>

F:112-135/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR3>

F:136-160/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR4>

F:161-186/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR5>

F:187-209/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR6>

F:210-232/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR7>

F:233-255/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR8>

F:256-279/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR9>

F:280-299/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR10>

F:300-323/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR11>

F:324-346/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR12>

F:363-386/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR14>

F:387-410/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR15>

F:411-434/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR16>

F:480-503/Domain: transmembrane #status_predicted <TM>

F:586-872/Domain: protein kinase homology <KIN>

F:594-602/Region: protein kinase ATP-binding motif

F:86_99,158,164,171,363,533,587/Binding site: carbohydrate (Asn) (covalent) #status_predicted

F:616,634,717,719/Active site: Lys, Glu, Asp, Lys #status_predicted

RESULT 13
S38149
SIS2 protein - yeast (*Saccharomyces cerevisiae*)
N/Alternate names: protein YKR072C
C/Species: *Saccharomyces cerevisiae*
C/Date: 03-May-1994 #sequence revision 03-May-1994 #text_change 09-Jul-2004
C/Accession: S38149; S54982; S43078
R:Pohl, T.M.; Pohl, F.M.
submitted to the Protein Sequence Database, March 1994
A/Reference number: S37897
A/Accession: S38149
A/Molecule type: DNA
A/Residues: 1-562 <POH>
A/Cross-references: UNIPROT:P36024; EMBL:Z28297; NID:g486544; PID:g486545; MIPS:YKR072C
A/Experimental source: strain S288C
R:di Como, C.J.; Bose, R.; Arndt, K.T.
Genetics 139, 95-107, 1995
A/Title: Overexpression of SIS2, which contains an extremely acidic region, increases the
A/Reference number: S54982; MUID:95220693; PMID:7705654
A/Accession: S54982
A/Molecule type: DNA
A/Residues: 1-562 <DIW>
A/Cross-references: EMBL:U01878; NID:q430983; PIDN:AAA80000.1; PID:g430984

GenBank: 1337, 93-1071, 1393
 A:Title: Overexpression of SIS2, which contains an extremely acidic region, increases the
 A:Reference number: S54982; MUID:95220693; PMID:7705654
 A:Accession: S54982
 A:Molecule type: DNA
 A:Residues: 1-562 <DIW>
 A:Cross-references: ENBL:U01878; NID:q430983; PIDN:AAA80000.1; PID:q430984

[illegible]

BEST AVAILABLE COPY
KIN7B LEFT PAGE SHL

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 1, 2005, 09:38:08 ; Search time 91 Seconds
(without alignments)
497.627 Million cell updates/sec

Title: US-10-617-876-3

Perfect score: 666

Sequence: 1 MANKTQPIITSTANKIWSDDTAA.....NAGLGFLDPTAAIVSSDTTA 131

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1465611 seqs, 345679903 residues

Total number of hits satisfying chosen parameters: 1465611

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
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17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	666	100.0	131	14	US-10-243-739-81 Sequence 81, Appl
2	666	100.0	131	14	US-10-244-065-81 Sequence 81, Appl
3	666	100.0	131	14	US-10-289-454-81 Sequence 81, Appl
4	666	100.0	131	15	US-10-346-190-96 Sequence 96, Appl
5	666	100.0	131	15	US-10-465-811-93 Sequence 93, Appl
6	666	100.0	131	15	US-10-289-456-113 Sequence 113, Appl
7	666	100.0	131	15	US-10-622-064-18 Sequence 18, Appl
8	666	100.0	131	15	US-10-617-876-3 Sequence 3, Appl
9	666	100.0	131	15	US-10-622-124-29 Sequence 29, Appl
10	666	100.0	131	16	US-10-622-087-29 Sequence 29, Appl
11	660	99.1	131	14	US-10-243-739-80 Sequence 80, Appl
12	660	99.1	131	14	US-10-244-065-80 Sequence 80, Appl
13	660	99.1	131	14	US-10-289-454-80 Sequence 80, Appl

14	660	99.1	131	15	US-10-346-190-95	Sequence 95, Appl
15	660	99.1	131	15	US-10-465-811-90	Sequence 90, Appl
16	660	99.1	131	15	US-10-289-456-112	Sequence 112, Appl
17	660	99.1	131	15	US-10-622-064-14	Sequence 14, Appl
18	660	99.1	131	15	US-10-617-876-1	Sequence 1, Appl
19	660	99.1	131	15	US-10-622-124-28	Sequence 28, Appl
20	660	99.1	131	16	US-10-622-087-28	Sequence 28, Appl
21	83.5	12.5	1619	16	US-10-437-963-121378	Sequence 121378,
22	81.5	12.2	662	16	US-10-437-963-121381	Sequence 121381,
23	81.5	12.2	1163	16	US-10-437-963-121376	Sequence 121376,
24	80	12.0	194	14	US-10-080-170-161	Sequence 161, App
25	80	12.0	194	16	US-10-080-170-161	Sequence 161, App
26	80	12.0	194	16	US-10-468-358-161	Sequence 161, App
27	79	11.9	329	16	US-10-755-889-426	Sequence 426, App
28	79	11.9	332	9	US-09-313-942-10	Sequence 10, Appl
29	79	11.9	332	9	US-09-935-868-10	Sequence 10, Appl
30	79	11.9	332	14	US-10-287-035-10	Sequence 10, Appl
31	79	11.9	332	14	US-10-282-162-10	Sequence 10, Appl
32	79	11.9	488	13	US-10-079-625-5	Sequence 5, Appl
33	79	11.9	708	14	US-10-313-135-2	Sequence 2, Appl
34	79	11.9	807	15	US-10-311-473-12	Sequence 12, Appl
35	79	11.9	859	9	US-09-313-942-7	Sequence 7, Appl
36	79	11.9	859	9	US-09-935-868-7	Sequence 7, Appl
37	79	11.9	859	14	US-10-287-035-7	Sequence 7, Appl
38	79	11.9	859	14	US-10-282-162-7	Sequence 7, Appl
39	79	11.9	918	10	US-09-853-180-4	Sequence 4, Appl
40	79	11.9	918	10	US-09-972-708-8	Sequence 8, Appl
41	79	11.9	918	14	US-10-177-293-230	Sequence 230, App
42	79	11.9	918	15	US-10-295-027-74	Sequence 74, Appl
43	79	11.9	918	15	US-10-058-270A-32	Sequence 32, Appl
44	79	11.9	918	16	US-10-715-667-8	Sequence 8, Appl
45	79	11.9	918	17	US-10-850-270-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1

US-10-243-739-81
; Sequence 81, Application US/10243739
; Publication No. US20030091593A1
; GENERAL INFORMATION:
; APPLICANT: Bachmann, Martin F.
; APPLICANT: Stornli, Tazio
; APPLICANT: Lechner, Franziska
; TITLE OF INVENTION: In vivo Activation of Antigen Presenting Cells for Enhancement of
; FILE REFERENCE: 1700.0210001
; CURRENT APPLICATION NUMBER: US/10/243,739
; PRIOR FILING DATE: 2002-09-16
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 81
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: AP205 coat protein
US-10-243-739-81

Query Match 100.0%; Score 666; DB 14; Length 131;
Best Local Similarity 100.0%; Pred. No. 3.6e-71;
Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MANKTQPIITSTANKIWSDDPTLSLTFSSASLRQVRKVGIAELNNVSGGVSVYKRPAP 60

Db 1 MANKTQPIITSTANKIWSDDPTLSLTFSSASLRQVRKVGIAELNNVSGGVSVYKRPAP 60

QY 61 KPEGCCADACVIMPENQSIPTVSSAENLATLKAETHKRVNVDTLFASGNAGLGFLDP 120

Db 61 KPEGCCADACVIMPENQSIPTVSSAENLATLKAETHKRVNVDTLFASGNAGLGFLDP 120


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QY 121 TAAIVSSDTTA 131
Db 121 TAAIVSSDTTA 131

RESULT 5
US-10-465-811-93
; Sequence 93, Application US/10465811
; Publication No. US20040005338A1
; GENERAL INFORMATION:
; APPLICANT: BACHMANN, MARTIN F
; APPLICANT: RENNER, WOLFGANG A
; TITLE OF INVENTION: PACKAGED VIRUS-LIKE PARTICLES FOR USE AS ADJUVANTS:
; TITLE OF INVENTION: METHOD OF PREPARATION AND USE
; FILE REFERENCE: 1700.0290004
; CURRENT APPLICATION NUMBER: US/10/465,811
; PRIOR FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: US 60/389,898
; PRIOR FILING DATE: 2002-06-20
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 93
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Bacteriophage AP205 mutant
US-10-465-811-93

Query Match 100.0%; Score 666; DB 15; Length 131;
Best Local Similarity 100.0%; Pred. No. 3.6e-71;
Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MANKTWPITSTANKIWMSPDTRLSTTFSASLLRQVRKVGVIAELNNVSGQYVSVYKRPAP 60

QY 61 KPEGCADACVIMPENQSIPTVIGSAENLATLKAETHKRNVDTLFASGNAGLGFLOP 120
Db 61 KPEGCADACVIMPENQSIPTVIGSAENLATLKAETHKRNVDTLFASGNAGLGFLOP 120

QY 121 TAAIVSSDTTA 131
Db 121 TAAIVSSDTTA 131

RESULT 6
US-10-289-456-113
; Sequence 113, Application US/10289456
; Publication No. US20040033211A1
; GENERAL INFORMATION:
; APPLICANT: Bachmann, Martin
; APPLICANT: Maurer, Patrick
; APPLICANT: Spohn, Gunther
; TITLE OF INVENTION: Antigen Arrays for Treatment of Bone Disease
; FILE REFERENCE: 1700.0330001
; CURRENT APPLICATION NUMBER: US/10/289,456
; CURRENT FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: PCT/IB02/00166
; PRIOR FILING DATE: 2002-01-21
; PRIOR APPLICATION NUMBER: US 10/050,902
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/396,635
; PRIOR FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: US 60/331,045
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 113
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Artificial Sequence
US-10-289-456-113

QY 1 MANKTWPITSTANKIWMSPDTRLSTTFSASLLRQVRKVGVIAELNNVSGQYVSVYKRPAP 60
Db 1 MANKTWPITSTANKIWMSPDTRLSTTFSASLLRQVRKVGVIAELNNVSGQYVSVYKRPAP 60

QY 61 KPEGCADACVIMPENQSIPTVIGSAENLATLKAETHKRNVDTLFASGNAGLGFLOP 120
Db 61 KPEGCADACVIMPENQSIPTVIGSAENLATLKAETHKRNVDTLFASGNAGLGFLOP 120

QY 121 TAAIVSSDTTA 131
Db 121 TAAIVSSDTTA 131

RESULT 7
US-10-622-064-18
; Sequence 18, Application US/10622064
; Publication No. US20040059094A1
; GENERAL INFORMATION:
; APPLICANT: Bachmann, Martin F
; APPLICANT: Maurer, Patrick F
; TITLE OF INVENTION: Hapten-Carrier Conjugates and Uses Thereof
; FILE REFERENCE: 1700.0300001
; CURRENT APPLICATION NUMBER: US/10/622,064
; CURRENT FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: US 60/396,575
; PRIOR FILING DATE: 2002-07-18
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Bacteriophage AP205 mutant
US-10-622-064-18

Query Match 100.0%; Score 666; DB 15; Length 131;
Best Local Similarity 100.0%; Pred. No. 3.6e-71;
Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MANKTWPITSTANKIWMSPDTRLSTTFSASLLRQVRKVGVIAELNNVSGQYVSVYKRPAP 60
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QY 61 KPEGCADACVIMPENQSIPTVIGSAENLATLKAETHKRNVDTLFASGNAGLGFLOP 120
Db 61 KPEGCADACVIMPENQSIPTVIGSAENLATLKAETHKRNVDTLFASGNAGLGFLOP 120

QY 121 TAAIVSSDTTA 131
Db 121 TAAIVSSDTTA 131

RESULT 8
US-10-617-876-3
; Sequence 3, Application US/10617876
; Publication No. US20040076611A1
; GENERAL INFORMATION:
; APPLICANT: Bachmann, Martin F
; APPLICANT: Tissot, Alain
; APPLICANT: Pumpsens, Paul
; APPLICANT: Cielens, Indulis
; APPLICANT: Renhofs, Regina
; TITLE OF INVENTION: Molecular Antigen Arrays
; FILE REFERENCE: 1700.0310001
US-10-617-876-3

; FEATURE:
; OTHER INFORMATION: AP205 coat protein
US-10-289-456-113

Query Match 100.0%; Score 666; DB 15; Length 131;
Best Local Similarity 100.0%; Pred. No. 3.6e-71;
Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MANKTWPITSTANKIWMSPDTRLSTTFSASLLRQVRKVGVIAELNNVSGQYVSVYKRPAP 60
Db 1 MANKTWPITSTANKIWMSPDTRLSTTFSASLLRQVRKVGVIAELNNVSGQYVSVYKRPAP 60

QY 61 KPEGCADACVIMPENQSIPTVIGSAENLATLKAETHKRNVDTLFASGNAGLGFLOP 120
Db 61 KPEGCADACVIMPENQSIPTVIGSAENLATLKAETHKRNVDTLFASGNAGLGFLOP 120

QY 121 TAAIVSSDTTA 131
Db 121 TAAIVSSDTTA 131
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Qy 1 MANKTQPIITSTANKIIVMSDPTRLSTTFSASLLRQVRKVGIAELNNVSGQYVSVYKRPAP 60
Db 1 MANKTQPIITSTANKIIVMSDPTRLSTTFSASLLRQVRKVGIAELNNVSGQYVSVYKRPAP 60
Qy 61 KPGCADACVIMPNENOSIRTVISGSAENLATLKAETHKRNVDTLFASGNAGLGFLDP 120
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Qy 121 TAAIVSSDTTA 131
Db 121 TAAIVSSDTTA 131

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RESULT 15
US-10-465-811-90
; Sequence 90, Application US/10465811
; Publication No. US20040005338A1
; GENERAL INFORMATION:
; APPLICANT: BACHMANN, MARTIN F
; TITLE OF INVENTION: PACKAGED VIRUS-LIKE PARTICLES FOR USE AS ADJUVANTS:
; FILE REFERENCE: 1700.0290004
; CURRENT APPLICATION NUMBER: US/10/465,811
; PRIOR FILING DATE: 2003-06-20
; PRIOR FILING DATE: 2002-06-20
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 90
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Bacteriophage AP205
US-10-465-811-90

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Query Match 99.1%; Score 660; DB 15; Length 131;
Best Local Similarity 99.2%; Pred. No. 1.9e-70;
Matches 130; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 MANKTQPIITSTANKIIVMSDPTRLSTTFSASLLRQVRKVGIAELNNVSGQYVSVYKRPAP 60
Db 1 MANKTQPIITSTANKIIVMSDPTRLSTTFSASLLRQVRKVGIAELNNVSGQYVSVYKRPAP 60
Qy 61 KPGCADACVIMPNENOSIRTVISGSAENLATLKAETHKRNVDTLFASGNAGLGFLDP 120
Db 61 KPGCADACVIMPNENOSIRTVISGSAENLATLKAETHKRNVDTLFASGNAGLGFLDP 120
Qy 121 TAAIVSSDTTA 131
Db 121 TAAIVSSDTTA 131

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Search completed: June 1, 2005, 09:51:00
Job time : 92 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 1, 2005, 09:35:42 ; Search time 30 Seconds
(without alignments)
325.968 Million cell updates/sec

Title: US-10-617-876-3

Perfect score: 666

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

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- 3: /cgn2_6/prodata/1/iaa/6A COMB pep.*
- 4: /cgn2_6/prodata/1/iaa/6B COMB pep.*
- 5: /cgn2_6/prodata/1/iaa/6C COMB pep.*
- 6: /cgn2_6/prodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	79	11.9	488	2	US-08-599-455B-5
3	79	11.9	488	3	US-09-069-781B-5
4	79	11.9	488	3	US-09-137-132-5
5	79	11.9	488	3	US-08-864-564A-5
6	79	11.9	488	4	US-09-094-410-5
7	79	11.9	488	4	US-08-708-123D-5
8	79	11.9	488	4	US-08-583-153A-5
9	79	11.9	488	4	US-08-638-524B-5
10	79	11.9	658	2	US-08-825-558-4
11	79	11.9	658	3	US-09-312-611-4
12	79	11.9	708	1	US-07-797-556-2
13	79	11.9	708	1	US-08-308-881-2
14	79	11.9	708	2	US-09-058-263-2
15	79	11.9	708	2	US-09-059-099-2
16	79	11.9	708	3	US-09-058-264-2
17	79	11.9	708	4	US-09-455-962-2
18	79	11.9	708	5	PCT-US95-06530-2
19	79	11.9	859	4	US-09-313-942-7
20	79	11.9	918	2	US-08-825-558-6
21	79	11.9	918	3	US-09-312-611-6
22	79	11.9	918	4	US-09-853-180B-3
23	79	11.9	951	4	US-09-313-942-9
24	79	11.9	1158	4	US-09-313-942-26
25	79	11.9	1168	4	US-09-313-942-24
26	79	11.0	488	4	US-09-252-991A-28535
27	72	10.8	185	4	US-09-252-991A-31599

28 70.5 10.6 248 4 US-09-252-991A-20247 Sequence 20247, A
29 70.5 10.6 5087 3 US-09-144-085-1 Sequence 1, Appli
30 70.5 10.6 6095 3 US-09-144-085-2 Sequence 2, Appli
31 70 10.5 179 4 US-09-270-767-43725 Sequence 43725, A
32 70 10.5 520 4 US-09-461-325-144 Sequence 144, App
33 70 10.5 520 4 US-10-012-542-144 Sequence 144, App
34 70 10.5 520 4 US-10-115-123-144 Sequence 144, App
35 69 10.4 414 4 US-09-489-039A-13320 Sequence 13320, A
36 67.5 10.1 300 4 US-09-252-991A-19422 Sequence 19422, A
37 67.5 10.1 343 3 US-08-858-003-32 Sequence 32, Appl
38 67.5 10.1 343 3 US-09-078-166-32 Sequence 32, Appl
39 67.5 10.1 343 3 US-08-997-467-32 Sequence 32, Appl
40 67 10.1 707 4 US-09-021-560-4 Sequence 4, Appli
41 67 10.1 707 4 US-09-202-178A-4 Sequence 4, Appli
42 66.5 10.0 480 4 US-09-710-279-2852 Sequence 2852, Ap
43 66.5 10.0 480 4 US-09-710-279-2986 Sequence 2986, Ap
44 66.5 10.0 490 3 US-09-134-001C-4019 Sequence 4019, Ap
45 66 9.9 287 4 US-09-292-858B-25 Sequence 25, Appl

ALIGNMENTS

RESULT 1

US-09-313-942-10

; Sequence 10, Application US/09313942

; Patent No. 6472179

; GENERAL INFORMATION:

; APPLICANT: REGENERON PHARMACEUTICALS, INC.

; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING

; TITLE OF INVENTION: AND USING

; FILE REFERENCE: REG 203-A

; CURRENT APPLICATION NUMBER: US/09/313,942

; CURRENT FILING DATE: 1999-05-19

; PRIOR APPLICATION NUMBER: 09/313,942

; PRIOR FILING DATE: 1999-05-19

; PRIOR APPLICATION NUMBER: 60/101,858

; PRIOR FILING DATE: 1998-09-25

; NUMBER OF SEQ ID NOS: 32

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 10

; LENGTH: 332

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-313-942-10

Query Match 11.9%; Score 79; DB 4; Length 332;

Best Local Similarity 25.5%; Pred. No. 0.35; Indels 16; Gaps 5;

Matches 25; Conservative 21; Mismatches 36; Indels 16; Gaps 5;

QY 9 ITSTANKIYMSDPTRLSTTFSASLLR-ORVKVGIAGLNNSGVYVYKRPAPKPEGCAD 67

DB 82 INRTASSVFTDIASLNILQTCNLTFGLEQNVYGITISG-----LPPEKPKNL-- 132

QY 68 ACVIMPNQSTRTVISGSAENLA-----TLKAEWETHK 101

DB 133 SCIV--NEGKRCRCEWDGGRETHLETNFTLKSEWATHK 168

RESULT 2

US-08-599-455B-5

; Sequence 5, Application US/08599455B

; Patent No. 5972621

; GENERAL INFORMATION:

; APPLICANT: Tartaglia, Louis A.

; APPLICANT: Tepper, Robert I.

; APPLICANT: Culpepper, Janice A.

; TITLE OF INVENTION: METHODS OF IDENTIFYING COMPOUNDS THAT

; TITLE OF INVENTION: MODULATE BODY WEIGHT USING THE OB RECEPTOR

; NUMBER OF SEQUENCES: 44

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson, P.C.

; STREET: 225 Franklin Street


```

; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/599,455B
; FILING DATE: 22-JAN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/583,153
; FILING DATE: 28-DEC-1995
; APPLICATION NUMBER: 08/570,142
; FILING DATE: 11-DEC-1995
; APPLICATION NUMBER: 08/569,485
; FILING DATE: 08-DEC-1995
; APPLICATION NUMBER: 08/566,622
; FILING DATE: 04-DEC-1995
; APPLICATION NUMBER: 08/562,663
; FILING DATE: 27-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Meiklejohn, Ph.D., Anita L.
; REGISTRATION NUMBER: 35,283
; REFERENCE/DOCKET NUMBER: 07334/017001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 488 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-599-455B-5

Query Match 11.9%; Score 79; DB 2; Length 488;
Best Local Similarity 25.5%; Pred. No. 0.62;
Matches 25; Conservative 21; Mismatches 36; Indels 16; Gaps 5;

Qy 9 ITSTANKIVNSDPRLSTTFSSASLIR-ORVKVGIAELNNVSGQVSVYKRPAPKPECCAD 67
Db 53 INRTASSVTFTDIASLNQLTNCNLTGQLEQNVYGITIISG-----LPPEKPKNL-- 103
Qy 68 ACVIMPNENOSIRTVISGSAENLA-----TLKAEWETHK 101
Db 104 SCIV--NEGKKMRCWDGGRHLETFNLTLSKSEWATHK 139

RESULT 3
US-09-069-781B-5
; Sequence 5, Application US/09069781B
; Patent No. 6287782
; GENERAL INFORMATION:
; APPLICANT: Tartaglia, Louis A.
; APPLICANT: Tepper, Robert I.
; APPLICANT: Culpepper, Janice A.
; APPLICANT: White, David W.
; TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR
; TITLE OF INVENTION: THE DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS,
; TITLE OF INVENTION: INCLUDING OBESITY AND CACHEXIA
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:

; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/599,455B
; FILING DATE: 22-JAN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/583,153
; FILING DATE: 28-DEC-1995
; APPLICATION NUMBER: 08/570,142
; FILING DATE: 11-DEC-1995
; APPLICATION NUMBER: 08/569,485
; FILING DATE: 08-DEC-1995
; APPLICATION NUMBER: 08/566,622
; FILING DATE: 04-DEC-1995
; APPLICATION NUMBER: 08/562,663
; FILING DATE: 27-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Meiklejohn, Ph.D., Anita L.
; REGISTRATION NUMBER: 35,283
; REFERENCE/DOCKET NUMBER: 07334/017001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 488 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-069-781B-5

Query Match 11.9%; Score 79; DB 3; Length 488;
Best Local Similarity 25.5%; Pred. No. 0.62;
Matches 25; Conservative 21; Mismatches 36; Indels 16; Gaps 5;

Qy 9 ITSTANKIVNSDPRLSTTFSSASLIR-ORVKVGIAELNNVSGQVSVYKRPAPKPECCAD 67
Db 53 INRTASSVTFTDIASLNQLTNCNLTGQLEQNVYGITIISG-----LPPEKPKNL-- 103
Qy 68 ACVIMPNENOSIRTVISGSAENLA-----TLKAEWETHK 101
Db 104 SCIV--NEGKKMRCWDGGRHLETFNLTLSKSEWATHK 139

RESULT 4
US-09-137-132-5
; Sequence 5, Application US/09137132
; Patent No. 6380363
; GENERAL INFORMATION:
; APPLICANT: Tartaglia, Louis A.
; APPLICANT: Tepper, Robert I.
; APPLICANT: Culpepper, Janice A.
; APPLICANT: White, David W.
; TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR
; TITLE OF INVENTION: THE DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS,
; TITLE OF INVENTION: INCLUDING OBESITY AND CACHEXIA
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:

```


CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/583,153A
FILING DATE: 28-DEC-1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/570,142
FILING DATE: 11-DEC-1995
APPLICATION NUMBER: 08/569,485
FILING DATE: 08-DEC-1995
APPLICATION NUMBER: 08/566,622
FILING DATE: 04-DEC-1995
APPLICATION NUMBER: 08/562,663
FILING DATE: 27-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Meiklejohn, Anita L.
REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 07334/016001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 488 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-583-153A-5

Query Match 11.9%; Score 79; DB 4; Length 488;
Best Local Similarity 25.5%; Pred. No. 0.62;
Matches 25; Conservative 21; Mismatches 36; Indels 16; Gaps 5;

QY 9 ITSTAKIVMSDPTRLSTTFSASLLR-QRVKVGIAELNNVSGQVSVYKRPAPKPGSCAD 67
Db 53 INRTASVTTDASLNLIQTCLNLTFGQEQNVGITIISG-----LPPEKPKNL-- 103
QY 68 ACVMPNENOSIRTVISGSAENLA----TLKAEWETHK 101
Db 104 SCIV--NEGKKMRCWDGGRETHLENTFTLKSEWATHK 139

RESULT 9
US-08-638-524B-5
Sequence 5, Application US/08638524B
Patent No. 6548269
GENERAL INFORMATION:
APPLICANT: Tartaglia, Louis A.
APPLICANT: Pepper, Robert I.
APPLICANT: Culpepper, Janice A.
APPLICANT: White, David W.
TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR THE
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING OB
TITLE OF INVENTION: CACHEXIA
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804

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; APPLICATION NUMBER: US/08/825,558
; FILING DATE: 19-MAR-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: ESMOND, ROBERT W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 0623.0530001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)371-2600
; TELEFAX: (202)371-2540
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 658 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-825-558--4

Query Match 11.9%; Score 79; DB 2; Length 658;
Best Local Similarity 25.5%; Pred. No. 0.98;
Matches 25; Conservative 21; Mismatches 36; Indels 16; Gaps 5;

Qy 9 ITSTANKIWMSDPTRLSTTFSASLLR-QRVKVGIAELNNVSGQVSVYKRPAPKPEGCAD 67
Db 82 INRTASSVTFTDIASLNQITCNILTFGQLEQNVYGITIISG-----LPPEKPKNL-- 132

Qy 68 ACVIMPNENQSIPTVSGSAENLA-----TLKAEWETHK 101
Db 133 SCIV--NEGKKMRCEWDGGRETHLETFNFTLKSEWATHK 168

RESULT 11
US-09-312-611-4
; Sequence 4, Application US/09312611
; Patent No. 6380160
; GENERAL INFORMATION:
; APPLICANT: SHARKEY, ANDREW
; APPLICANT: SMITH, STEPHEN K.
; APPLICANT: DELLOW, KIMBERLEY A.
; TITLE OF INVENTION: Gp130 Lacking the Transmembrane Domain
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX
; STREET: 1100 NEW YORK AVENUE
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 17-MAY-1999
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: ESMOND, ROBERT W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 0623.0530002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)371-2600
; TELEFAX: (202)371-2540
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 658 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-312-611-4

Query Match 11.9%; Score 79; DB 3; Length 658;
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Best Local Similarity 25.5%; Pred. No. 0.98;
Matches 25; Conservative 21; Mismatches 36; Indels 16; Gaps 5;

Qy 9 ITSTANKIWMSDPTRLSTTFSASLLR-QRVKVGIAELNNVSGQVSVYKRPAPKPEGCAD 67
Db 82 INRTASSVTFTDIASLNQITCNILTFGQLEQNVYGITIISG-----LPPEKPKNL-- 132

Qy 68 ACVIMPNENQSIPTVSGSAENLA-----TLKAEWETHK 101
Db 133 SCIV--NEGKKMRCEWDGGRETHLETFNFTLKSEWATHK 168

RESULT 12
US-07-797-556-2
; Sequence 2, Application US/07797556
; Patent No. 5262522
; GENERAL INFORMATION:
; APPLICANT: Gearing, David P.
; TITLE OF INVENTION: Receptor for Oncostatin M and Leukemia
; TITLE OF INVENTION: Inhibitory Factor
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 19911122
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Seese, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2607
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-587-0430
; TELEFAX: 206-587-0606
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 708 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-797-556-2

Query Match 11.9%; Score 79; DB 1; Length 708;
Best Local Similarity 25.5%; Pred. No. 1.1;
Matches 25; Conservative 21; Mismatches 36; Indels 16; Gaps 5;

Qy 9 ITSTANKIWMSDPTRLSTTFSASLLR-QRVKVGIAELNNVSGQVSVYKRPAPKPEGCAD 67
Db 82 INRTASSVTFTDIASLNQITCNILTFGQLEQNVYGITIISG-----LPPEKPKNL-- 132

Qy 68 ACVIMPNENQSIPTVSGSAENLA-----TLKAEWETHK 101
Db 133 SCIV--NEGKKMRCEWDGGRETHLETFNFTLKSEWATHK 168

RESULT 13
US-08-308-881-2
; Sequence 2, Application US/08308881
; Patent No. 5783672
; GENERAL INFORMATION:
; APPLICANT: Mosley, Bruce
; APPLICANT: Cosman, David J.
; TITLE OF INVENTION: Receptor for Oncostatin M
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; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 708 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-09-059-099-2

Query Match      11.9%; Score 79; DB 2; Length 708;
Best Local Similarity 25.5%; Pred. No. 1.1;
Matches 25; Conservative 21; Mismatches 36; Indels 16; Gaps 5;

Qy      9 ITSTANKIVWSDPTRLSTTFESALLR-ORVKVGIAELNNVSGQVSVYKRPAPKPEGCAD 67
Db      82 INRTASSVTFTDIASLNQLTCNLTFCQLEQNVYGITIISG-----LPPEKPKNL-- 132

Qy      68 ACVIMPENQSIKRTVISGSAENLA----TLKAEWETHK 101
Db      133 SCIV--NEGKMKRCMDGGRETHLETNFTLKSEWATHK 168
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Search completed: June 1, 2005, 09:47:52
Job time : 30 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 1, 2005, 09:31:22 ; Search time 114 Seconds
(without alignments)
444.435 Million cell updates/sec

Title: US-10-617-876-3

Perfect score: 666

Sequence: 1 MANKTQPTITSTANKIWSDD.....NAGLGFLDPTAALVSSDTTA 131

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : 1_Geneseq_16Dec04:*
2: Geneseqp1980s:*
3: Geneseqp1990s:*
4: Geneseqp2000s:*
5: Geneseqp2001s:*
6: Geneseqp2002s:*
7: Geneseqp2003as:*
8: Geneseqp2003bs:*
9: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	666	100.0	131	6	ABR56509 AP205 coa
2	666	100.0	131	6	ABU09695 Bacteriop
3	666	100.0	131	6	ABR44612 AP205 coa
4	666	100.0	131	7	ADD24203 Bacteriop
5	666	100.0	131	7	ADJ82146 Protein f
6	666	100.0	131	7	ADK17202 AP3 prote
7	666	100.0	131	8	ADJ36392 Bacteriop
8	666	100.0	131	8	ADI40712 Bacteriop
9	666	100.0	131	8	ADJ67171 Bacteriop
10	666	100.0	131	8	ADK52205 Bacteriop
11	666	100.0	131	8	ADL98305 Mutant Ba
12	660	99.1	131	6	ABR56508 AP205 coa
13	660	99.1	131	6	ABU09694 Bacteriop
14	660	99.1	131	6	ABR44611 AP205 coa
15	660	99.1	131	7	ADD24202 Bacteriop
16	660	99.1	131	7	ADJ82145 Protein f
17	660	99.1	131	7	ADK17201 API prote
18	660	99.1	131	8	ADJ36389 Bacteriop
19	660	99.1	131	8	ADI40710 Bacteriop
20	660	99.1	131	8	ADJ67170 Bacteriop
21	660	99.1	131	8	ADK52204 Bacteriop
22	660	99.1	131	8	ADL98301 Bacteriop
23	80	12.0	194	5	ABU05510 M. tuberc
24	79	11.9	329	2	AAW17859 Rheumatol
25	79	11.9	329	8	ADR14425 Human NF-

26	79	11.9	332	2	AAW70799	AAW70799 Human gp1
27	79	11.9	332	3	AAV92188	AAV92188 Human gp1
28	79	11.9	332	7	ABW02167	ABW02167 Human gp1
29	79	11.9	488	4	AAE12610	AAE12610 Human gp1
30	79	11.9	488	5	AAE23860	AAE23860 Human Ob
31	79	11.9	488	8	ADG62980	ADG62980 Human gp1
32	79	11.9	658	2	AAK94576	AAK94576 Human gp1
33	79	11.9	708	2	AAK37804	AAK37804 Human gp1
34	79	11.9	708	2	AAK85911	AAK85911 gp130 N-t
35	79	11.9	727	3	AAV92192	AAV92192 Human gp1
36	79	11.9	738	3	AAV92194	AAV92194 Human gp1
37	79	11.9	809	5	AAU75498	AAU75498 Human Int
38	79	11.9	859	2	AAW70796	AAW70796 Human gp1
39	79	11.9	859	3	AAV92184	AAV92184 Human gp1
40	79	11.9	859	7	ABW02164	ABW02164 Human gp1
41	79	11.9	918	2	AAK10545	AAK10545 Recombina
42	79	11.9	918	2	AAK46233	AAK46233 Human sol
43	79	11.9	918	2	AAK75368	AAK75368 Human gp1
44	79	11.9	918	3	AAV44694	AAV44694 Human gp1
45	79	11.9	918	5	ABJ05551	ABJ05551 Breast ca

ALIGNMENTS

RESULT 1

ABR56509

ID ABR56509 standard; protein; 131 AA.

XX AC ABR56509;

XX XX

DT 28-JUL-2003 (first entry)

XX XX

DE AP205 coat protein SEQ ID NO:81.

XX XX

KW Antigen presenting cell; APC; immune response; virus like particle; VLP;
KW cytostatic; virucide; antibacterial; antiparasitic; fungicide;

KW antiallergic; immunosuppressive; antiaddictive; antiinflammatory;

KW antithyroid; antidiabetic; neuroprotective; nootropic; osteopathic;

KW antirheumatic; antiarthritic; vaccine; immunisation; infectious disease;

KW anti-viral protection; tumour; allergy; drug addiction; Crohn's disease;

KW graft-versus-host disease; Grave's disease; diabetes; multiple sclerosis;

KW Alzheimer's disease; osteoporosis; rheumatoid arthritis;

KW inflammatory autoimmune disease.

XX XX

OS Synthetic.

XX XX

PN WO2003024480-A2.

XX XX

PD 27-MAR-2003.

XX XX

PF 16-SEP-2002; 2002WO-IB004252.

XX XX

PR 14-SEP-2001; 2001US-0318967P.

XX XX

PA (CYTO-) CYTOS BIOTECHNOLOGY AG.

XX XX

PI Bachmann MF, Storni T, Lechner F;

XX XX

DR WPI; 2003-363095/34.

XX XX

PT A composition, useful for enhancing an immune response against an antigen
or a virus-like particle, enhancing anti-viral protection in an animal,

PT or immunizing or treating tumors or infectious diseases, e.g. viral

PT infections.

XX XX

PS Disclosure; Page 240-241; 243pp; English.

XX XX

CC The present invention describes a composition (C) for enhancing an immune
response against an antigen or a virus-like particle in an animal. (C)

CC comprises a virus-like particle (VLP) bound to at least one antigen, or a

CC VLP capable of being recognised by the immune system of the animal. Also

CC described: (1) enhancing an immune response against an antigen or a VLP

CC in an animal comprising introducing (C) into the animal; (2) vaccines
 CC comprising (C) together with a pharmaceutical diluent, carrier or
 CC excipient; (3) immunising or treating an animal comprising administering
 CC the vaccine to the animal, or priming or boosting a T cell response in
 CC the animal by administering the vaccine; and (4) enhancing anti-viral
 CC protection in an animal comprising introducing (C) into the animal. (C)
 CC has cytostatic, virucide, antibacterial, antiparasitic, fungicide,
 CC antiallergic, immunosuppressive, antiaddictive, antiinflammatory,
 CC antithyroid, antidiabetic, neuroprotective, nootropic, osteopathic,
 CC antirheumatic and antiarthritic activities. (C) or the vaccines can be
 CC used for enhancing an immune response against an antigen or a VLP in an
 CC animal, enhancing anti-viral protection in an animal, or immunising or
 CC treating tumours and infectious diseases such as viral, bacterial,
 CC parasitic or fungal infections. The vaccine compositions are also useful
 CC for preventing or treating allergies, drug addiction, graft-versus-host
 CC disease, Crohn's disease, Grave's disease, diabetes, multiple sclerosis,
 CC Alzheimer's disease, osteoporosis, rheumatoid arthritis, or inflammatory
 CC autoimmune disease. ACC69838 to ACC69852 and ABR56401 to ABR56509
 CC represent sequences used in the exemplification of the present invention
 XX
 SQ Sequence 131 AA;

Query Match 100.0%; Score 666; DB 6; Length 131;
 Best Local Similarity 100.0%; Pred. No. 2e-72;
 Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MANKTQPIITSTANKIIVMSDPTRLSTTFSASLLRQVRKVGIAELNNVSGQVSVYKRPAP 60
 DB 1 MANKTQPIITSTANKIIVMSDPTRLSTTFSASLLRQVRKVGIAELNNVSGQVSVYKRPAP 60
 QY 61 KPEGCADACVIMPENQSIIRTVISGSAENLATLKAETHKRNVDTLFASGNAGLGFLDP 120
 DB 61 KPEGCADACVIMPENQSIIRTVISGSAENLATLKAETHKRNVDTLFASGNAGLGFLDP 120
 QY 121 TAAIVSSDTTA 131
 DB 121 TAAIVSSDTTA 131
 RESULT 2
 ABU09695
 ID ABU09695 standard; protein; 131 AA.
 AC ABU09695;
 DT 03-JUL-2003 (first entry)
 XX Bacteriophage AP205 coat protein mutant.
 XX Bacteriophage AP205; coat protein; hypotensive; cerebroprotective;
 KW cardiant; nephrotropic; ophthalmological; immunostimulant; vaccine;
 KW angiotensin peptide moiety carrier conjugate; angiotensin peptide;
 KW renin-activated angiotensin system; hypertension; stroke; infarction;
 KW congestive heart failure; kidney failure; retinal haemorrhage; mutant;
 KW mutein.
 XX Bacteriophage AP205.
 OS Bacteriophage AP205.

XX Key Location/Qualifiers
 FH Misc-difference 5
 FT /note= "Wild type Pro substituted by Thr"
 XX

PN WO2003031466-A2.
 XX 17-APR-2003.
 XX 07-OCT-2002; 2002WO-EP011219.
 XX 05-OCT-2001; 2001US-0326998P.
 PR 07-NOV-2001; 2001US-0331045P.
 PR 18-JAN-2002; 2002US-00050902.
 PR 21-JAN-2002; 2002WO-IB000166.
 PR 19-JUL-2002; 2002US-0396637P.

XX (CVTO-) CYTOS BIOTECHNOLOGY AG.
 PA Bachmann M;
 XX

XX WPI; 2003-430264/40.
 DR N-PSDB; ABX95524.
 XX

PT New angiotensin peptide moiety carrier conjugate comprising a carrier and
 an angiotensin peptide moiety, useful for treating or preventing a
 PT disorder associated with renin-activated angiotensin, e.g. hypertension
 or infarction.
 XX

PS Disclosure; Page 96; 97pp; English.

XX The invention describes an angiotensin peptide moiety carrier conjugate
 comprising: (a) a carrier with at least one first attachment site; and
 CC (b) at least one angiotensin peptide moiety with at least one second
 CC attachment site. The angiotensin peptide conjugate and compositions
 CC comprising them are useful for immunising an animal against an
 CC angiotensin peptide, and for treating or preventing a physical disorder
 CC associated with renin-activated angiotensin system such as hypertension,
 CC stroke, infarction, congestive heart failure, kidney failure, and retinal
 CC haemorrhage. The conjugate is also useful for inducing immune responses,
 CC including producing antibodies. This is the amino acid sequence of a
 CC bacteriophage AP205 coat protein mutant based on the wild type sequence
 CC shown in ABU09694 and used in the preparation of the vaccine conjugates
 CC of the invention
 XX

SQ Sequence 131 AA;

Query Match 100.0%; Score 666; DB 6; Length 131;
 Best Local Similarity 100.0%; Pred. No. 2e-72;
 Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MANKTQPIITSTANKIIVMSDPTRLSTTFSASLLRQVRKVGIAELNNVSGQVSVYKRPAP 60
 DB 1 MANKTQPIITSTANKIIVMSDPTRLSTTFSASLLRQVRKVGIAELNNVSGQVSVYKRPAP 60
 QY 61 KPEGCADACVIMPENQSIIRTVISGSAENLATLKAETHKRNVDTLFASGNAGLGFLDP 120
 DB 61 KPEGCADACVIMPENQSIIRTVISGSAENLATLKAETHKRNVDTLFASGNAGLGFLDP 120
 QY 121 TAAIVSSDTTA 131
 DB 121 TAAIVSSDTTA 131

RESULT 3
 ABR44612
 ID ABR44612 standard; protein; 131 AA.
 XX

AC ABR44612;

DT 25-JUL-2003 (first entry)

DE AP205 coat protein SEQ ID NO:81.

XX Immunostimulatory; virus-like particle; bacteriophage; HBV; LCMV;
 KW hepatitis B virus; lymphocytic choriomeningitis virus; vaccine;
 KW immunostimulant; cytostatic; antiallergic; virucide; antibacterial;
 KW immune response; immunisation; allergy; tumour; breast cancer;
 KW neuroblastoma; leukaemia; viral disease; influenza; hepatitis; measles;
 KW chicken pox; bacterial infection; tuberculosis; pneumonia; syphilis.

OS Synthetic.

PN WO2003024481-A2.

XX 27-MAR-2003.

XX 16-SEP-2002; 2002WO-IB004132.

PR 14-SEP-2001; 2001US-0318994P.
 PR 22-APR-2002; 2002US-0374145P.
 XX
 PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
 PA (MAUR/) MAURER P.
 PA (TISS/) TISSOT A.
 PA (SCHW/) SCHWARZ K.
 PA (MELJ/) MELJERINK E.
 PA (LIPO/) LIPOWSKY G.
 PA (PUMP/) PUMPENS P.
 PA (CIEL/) CIELENS I.
 PA (RENH/) RENHOFA R.
 XX
 PI Maurer P, Tissot A, Schwarz K, Meijerink E, Lipowsky G;
 PI Pumpens P, Cielens I, Renhofs R, Bachmann MF, Storni T;
 XX
 DR WPI; 2003-354564/33.
 XX
 PT New compositions comprising immunostimulatory substances packaged into
 PT virus-like particles, useful as a vaccine for enhancing an immune
 PT response in animals, e.g. for treating or preventing allergies, tumors or
 PT viral infections.
 XX
 PS Disclosure; Page 319-320; 322pp; English.
 XX
 CC The present invention describes a composition (C) for enhancing an immune
 CC response in an animal. (C) comprises a virus-like particle (VLP), and an
 CC immunostimulatory substance. The immunostimulatory substance is bound to
 CC the VLP. Also described: (1) enhancing an immune response in an animal by
 CC introducing (C) into the animal; (2) producing (C) for enhancing an
 CC immune response in an animal; (3) vaccines comprising (C) together with a
 CC pharmaceutical diluent, carrier or excipient; and (4) immunising or
 CC treating an animal by: (a) administering the vaccine to the animal; (b)
 CC priming a T cell response in the animal by administering the vaccine; or
 CC (c) boosting a T cell response in the animal by administering the
 CC vaccine. (C) has immunostimulant, cytostatic, antiallergic, virucide and
 CC antibacterial activities. (1) can be used in vaccines for enhancing an
 CC immune response in an animal, particularly a mammal or human.
 CC Specifically, (C) is useful for enhancing a B cell response, a T cell
 CC response, or a cytotoxic T-lymphocyte (CTL) response. (C) or a vaccine
 CC comprising (C) can also be used for immunising or treating an animal,
 CC e.g. humans, sheep, horses, cattle, pigs, dogs, cats, rats, birds,
 CC reptiles or fish. (C) is particularly useful in prophylactic or
 CC therapeutic vaccines against allergies, tumours (e.g. breast cancers,
 CC neuroblastoma, or leukaemia), viral diseases (e.g. influenza, hepatitis,
 CC measles or chicken pox), or bacterial infections (e.g. tuberculosis,
 CC pneumonia or syphilis). ACC69790 to ACC69815 and ABR44502 to ABR44612
 CC represent sequences used in the exemplification of the present invention
 XX
 SQ Sequence 131 AA;
 Query Match 100.0%; Score 666; DB 6; Length 131;
 Best Local Similarity 100.0%; Pred. No. 2e-72;
 Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MANKTQPIITSTANKIWSDPTRLSTTFSASLLRQKVGIAELNNVSGQVSVYKRPAP 60
 DB 1 MANKTQPIITSTANKIWSDPTRLSTTFSASLLRQKVGIAELNNVSGQVSVYKRPAP 60
 QY 61 KPFGCADACVIMPNENQSIPTVIGSGAENLATLKAETHKRNVDTLFASGNAGLGLDLP 120
 DB 61 KPFGCADACVIMPNENQSIPTVIGSGAENLATLKAETHKRNVDTLFASGNAGLGLDLP 120
 QY 121 TAAIVSSDTTA 131
 DB 121 TAAIVSSDTTA 131
 RESULT 4
 ADD24203
 ID ADD24203 standard; protein; 131 AA.
 XX
 AC ADD24203;

XX 15-JAN-2004 (first entry)
 XX Bacteriophage AP205 coat protein #2.
 DE vaccine composition; virus-like particle; core particle;
 XX first attachment site; antigen; antigenic determinant; prion protein;
 KW PrP; PrP peptide; vaccine; neuroprotective; antiinflammatory;
 KW prion disease; Bovine Spongiform Encephalopathy; BSE;
 KW Creutzfeldt-Jakob Disease; prion; AP205; coat protein.
 XX Synthetic.
 OS Bacteriophage AP205.
 XX WO2003059386-A2.
 PN 24-JUL-2003.
 XX
 XX 17-JAN-2003; 2003WO-EP000460.
 PF 19-JAN-2002; 2002US-00050902.
 PR 21-JAN-2002; 2002WO-1B000166.
 PR 08-JUL-2002; 2002US-0393725P.
 PR 18-JUL-2002; 2002US-0396590P.
 XX (CYTO-) CYTOS BIOTECHNOLOGY AG.
 PA Bachmann M, Maurer P, Pelliccioli E, Renner WA;
 PI WPI; 2003-598483/56.
 DR N-PSDB; ADD24204.
 XX
 XX A vaccine composition for preventing or treating prion diseases (e.g.
 PT Creutzfeldt-Jakob Disease) comprises a virus-like particle (e.g. RNA-
 PT phage) and at least one prion protein or peptide bound to the virus-like
 PT particle.
 XX Disclosure; SEQ ID NO 96; 246pp; English.
 PS This invention relates to a novel vaccine composition comprising a virus-
 CC like or a core particle with at least one first attachment site and at
 CC least one antigen or antigenic determinant that is a prion protein (PrP)
 CC or its dimer, or a PrP peptide, the antigen or antigenic determinant
 CC being bound to the virus-like or core particle. The vaccine of the
 CC invention may have neuroprotective or antiinflammatory activity. The
 CC composition is useful as a medicament or in manufacturing a medicament
 CC for the treatment or prevention of prion diseases. The prion diseases may
 CC include Bovine Spongiform Encephalopathy (BSE) or Creutzfeldt-Jakob
 CC Disease. The present sequence is that of a mutant RNA-phage AP205 coat
 CC protein which is related to the invention.
 XX
 SQ Sequence 131 AA;
 Query Match 100.0%; Score 666; DB 7; Length 131;
 Best Local Similarity 100.0%; Pred. No. 2e-72;
 Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MANKTQPIITSTANKIWSDPTRLSTTFSASLLRQKVGIAELNNVSGQVSVYKRPAP 60
 DB 1 MANKTQPIITSTANKIWSDPTRLSTTFSASLLRQKVGIAELNNVSGQVSVYKRPAP 60
 QY 61 KPFGCADACVIMPNENQSIPTVIGSGAENLATLKAETHKRNVDTLFASGNAGLGLDLP 120
 DB 61 KPFGCADACVIMPNENQSIPTVIGSGAENLATLKAETHKRNVDTLFASGNAGLGLDLP 120
 QY 121 TAAIVSSDTTA 131
 DB 121 TAAIVSSDTTA 131
 RESULT 5
 ADD242146
 ID ADJ82146 standard; protein; 131 AA.

XX AC ADJ67171;
 XX DT 06-MAY-2004 (first entry)
 XX DE Bacteriophage AP205 P5T mutant coat protein for antigen display array.
 XX KW anorectic; core particle; antigenic determinant; ghrelin; P-pilin;
 XX KW antigenic array.
 XX OS Bacteriophage AP205.
 XX PN WO2004009124-A2.
 XX PD 29-JAN-2004.
 XX PF 18-JUL-2003; 2003WO-EP007849.
 XX PR 19-JUL-2002; 2002US-0396638P.
 XX PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
 XX PI Bachmann MF, Fulurija A;
 XX PS WPI; 2004-132866/13.
 XX PT New composition comprising a core particle having a first attachment site
 PT and an antigen or antigenic determinant which is a ghrelin or ghrelin
 PT peptide having a second attachment site, useful for treating obesity.
 XX PS Disclosure; SEQ ID NO 29; 175pp; English.
 XX CC The invention relates to a new composition comprising: (i) a core
 CC particle with at least one first attachment site; and (ii) at least one
 CC antigen or antigenic determinant with at least one second attachment
 CC site, where the antigen or antigenic determinant is ghrelin or a ghrelin
 CC peptide, and where the second attachment site being consisting of an
 CC attachment site not naturally occurring with the antigen or antigenic
 CC determinant and an attachment site naturally occurring with the antigen
 CC or antigenic determinant, where the second attachment site is capable of
 CC association to the first attachment site, and where the ghrelin or a
 CC ghrelin peptide and the core particle interact through the association to
 CC form an ordered and repetitive antigen array. The composition is useful
 CC for treating obesity. The repetitive array may form part of a phage or
 CC bacterial display array. This peptide corresponds to a mutant
 CC Bacteriophage AP205 coat protein (Pro 5 changed to Thr) which can be used as
 XX part of the repetitive or antigenic array.
 XX SQ Sequence 131 AA;
 Query Match 100.0%; Score 666; DB 8; Length 131;
 Best Local Similarity 100.0%; Pred. No. 2e-72;
 Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MANKTMOPIITSTANKIWSDPTRLSTTFSASLLRQVRKVGLAEINNVSGQVSVYKRPAP 60
 DB 1 MANKTMOPIITSTANKIWSDPTRLSTTFSASLLRQVRKVGLAEINNVSGQVSVYKRPAP 60
 QY 61 KPEGCADACVIMPNENQSIPTVIGSGAENLATLKAWEETHKRNVDTLFASGNAGLGLDLP 120
 DB 61 KPEGCADACVIMPNENQSIPTVIGSGAENLATLKAWEETHKRNVDTLFASGNAGLGLDLP 120
 QY 121 TAAIVSSDDTTA 131
 DB 121 TAAIVSSDDTTA 131
 RESULT 10
 ADK52205
 ID ADK52205 standard; protein; 131 AA.
 XX ADK52205;
 XX

DT 20-MAY-2004 (first entry)
 XX Bacteriophage AP205 coat protein mutant P5T.
 XX DE neuroprotective; nootropic; vaccine; amyloid beta 1-6 peptide;
 XX KW core particle; antigen array; Alzheimer's disease; RNA bacteriophage;
 XX KW coat protein; mutant; mutein.
 XX OS Bacteriophage AP205.
 XX PN Synthetic.
 XX FT Key Location/Qualifiers
 FT Misc-difference 5 /note= "Wild type Pro substituted by Thr"
 XX WO2004016282-A1.
 XX PD 26-FEB-2004.
 XX PF 18-JUL-2003; 2003WO-EP007864.
 XX PR 19-JUL-2002; 2002US-0396639P.
 XX PR 15-MAY-2003; 2003US-0470432P.
 XX PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
 XX PA (NOVS) NOVARTIS PHARMA AG.
 XX PI Bachmann MF, Tissot A, Ortmann R, Lueoend R, Staufenbiel M;
 XX PI Frey P;
 XX PS WPI; 2004-203731/19.
 XX PT Composition comprising a core particle with at least one attachment site,
 PT and an antigenic amyloid beta 1-6 peptide, useful for treating diseases
 PT such as Alzheimer's disease.
 XX PS Example 1; SEQ ID NO 29; 184pp; English.
 XX CC The invention describes a novel composition comprising a core particle
 CC with at least one attachment site, and an antigenic amyloid beta 1-6
 CC peptide. The new composition comprises: a core particle with at least one
 CC first attachment site; and at least one antigen or antigenic determinant
 CC with at least one second attachment site, where the antigen or antigenic
 CC determinant is a Amyloid beta 1-6 peptide, and where the second
 CC attachment site comprises: an attachment site not naturally occurring
 CC with the antigen or antigenic determinant; or an attachment site
 CC naturally occurring with the antigen or antigenic determinant. The second
 CC attachment site is capable of association to the first attachment site
 CC and the beta 1-6 peptide and the core particle interact through the
 CC association to form an ordered and repetitive antigen array. The
 CC composition is useful for the manufacture of a medicament for treating
 CC Alzheimer's disease and related diseases. This is the amino acid sequence
 CC of an assembly-competent RNA bacteriophage AP205 mutant coat protein that
 CC can be used in the preparation of the compositions and vaccines of the
 XX invention.
 XX SQ Sequence 131 AA;
 Query Match 100.0%; Score 666; DB 8; Length 131;
 Best Local Similarity 100.0%; Pred. No. 2e-72;
 Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MANKTMOPIITSTANKIWSDPTRLSTTFSASLLRQVRKVGLAEINNVSGQVSVYKRPAP 60
 DB 1 MANKTMOPIITSTANKIWSDPTRLSTTFSASLLRQVRKVGLAEINNVSGQVSVYKRPAP 60
 QY 61 KPEGCADACVIMPNENQSIPTVIGSGAENLATLKAWEETHKRNVDTLFASGNAGLGLDLP 120
 DB 61 KPEGCADACVIMPNENQSIPTVIGSGAENLATLKAWEETHKRNVDTLFASGNAGLGLDLP 120
 QY 121 TAAIVSSDDTTA 131
 DB 121 TAAIVSSDDTTA 131

CC represent sequences used in the exemplification of the present invention

XX SQ Sequence 131 AA;

Query Match 99.1%; Score 660; DB 6; Length 131;
 Best Local Similarity 99.2%; Pred. No. 1.1e-71;
 Matches 130; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MANKTQPISTANKIWSDPTRLSTTFSSASLLRQVRKVGLAELNNVSGQVSVYKRPAP 60
 DB 1 MANKPMQPISTANKIWSDPTRLSTTFSSASLLRQVRKVGLAELNNVSGQVSVYKRPAP 60

QY 61 KPEGCADACVIMPNENOSIRTVISGSAENLATLKAETHKRNVDTLFASGNAGLGLDLP 120
 DB 61 KPEGCADACVIMPNENOSIRTVISGSAENLATLKAETHKRNVDTLFASGNAGLGLDLP 120

QY 121 TAAIVSSDTTA 131
 DB 121 TAAIVSSDTTA 131

RESULT 13

ABU09694
 ID ABU09694 standard; protein; 131 AA.
 AC ABU09694;
 XX
 DT 03-JUL-2003 (first entry)
 XX
 DE Bacteriophage AP205 coat protein.
 XX
 KW Bacteriophage AP205; coat protein; hypotensive; cerebroprotective;
 KW cardiant; nephrotropic; ophthalmological; immunostimulant; vaccine;
 KW angiotensin peptide moiety carrier conjugate; angiotensin peptide;
 KW renin-activated angiotensin system; hypertension; stroke; infarction;
 KW congestive heart failure; kidney failure; retinal haemorrhage.
 XX
 OS Bacteriophage AP205.
 XX
 PN W02003031466-A2.
 XX
 PD 17-APR-2003.
 XX
 PF 07-OCT-2002; 2002WO-EP011219.
 XX
 PR 05-OCT-2001; 2001US-0326998P.
 PR 07-NOV-2001; 2001US-0331045P.
 PR 18-JAN-2002; 2002US-00050902.
 PR 21-JAN-2002; 2002WO-IB000166.
 PR 19-JUL-2002; 2002US-0396637P.
 XX
 PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
 XX
 PI Bachmann M;
 XX
 WPI: 2003-430264/40.
 DR N-PSDB; ABX95523.
 DR
 DR
 DR
 XX New angiotensin peptide moiety carrier conjugate comprising a carrier and
 PT an angiotensin peptide moiety, useful for treating or preventing a
 PT disorder associated with renin-activated angiotensin, e.g. hypertension
 PT or infarction.
 XX
 XX Disclosure; Page 96; 97pp; English.

The invention describes an angiotensin peptide moiety carrier conjugate comprising: (a) a carrier with at least one first attachment site; and (b) at least one angiotensin peptide moiety with at least one second attachment site. The angiotensin peptide moiety carrier conjugate and compositions comprising them are useful for immunising an animal against an angiotensin peptide, and for treating or preventing a physical disorder associated with renin-activated angiotensin system such as hypertension, stroke, infarction, congestive heart failure, kidney failure, and retinal

CC haemorrhage. The conjugate is also useful for inducing immune responses, including producing antibodies. This is the amino acid sequence of a bacteriophage AP205 coat protein used in the preparation of the vaccine conjugates of the invention

XX SQ Sequence 131 AA;

Query Match 99.1%; Score 660; DB 6; Length 131;
 Best Local Similarity 99.2%; Pred. No. 1.1e-71;
 Matches 130; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MANKTQPISTANKIWSDPTRLSTTFSSASLLRQVRKVGLAELNNVSGQVSVYKRPAP 60
 DB 1 MANKPMQPISTANKIWSDPTRLSTTFSSASLLRQVRKVGLAELNNVSGQVSVYKRPAP 60

QY 61 KPEGCADACVIMPNENOSIRTVISGSAENLATLKAETHKRNVDTLFASGNAGLGLDLP 120
 DB 61 KPEGCADACVIMPNENOSIRTVISGSAENLATLKAETHKRNVDTLFASGNAGLGLDLP 120

QY 121 TAAIVSSDTTA 131
 DB 121 TAAIVSSDTTA 131

RESULT 14

ABR44611
 ID ABR44611 standard; protein; 131 AA.
 XX ABR44611;
 AC ABR44611;
 XX
 DT 25-JUL-2003 (first entry)
 XX
 DE AP205 coat protein SEQ ID NO:80.
 XX
 KW Immunostimulatory; virus-like particle; bacteriophage; HBV; LCMV;
 KW hepatitis B virus; lymphocytic choriomeningitis virus; vaccine;
 KW immunostimulant; cytostatic; antiallergic; virucide; antibacterial;
 KW immune response; leukaemia; allergy; tumour; breast cancer;
 KW neuroblastoma; viral disease; influenza; hepatitis; measles;
 KW chicken pox; bacterial infection; tuberculosis; pneumonia; syphilis.
 XX
 OS Synthetic.
 XX
 PN W02003024481-A2.
 XX
 PD 27-MAR-2003.
 XX
 PF 16-SEP-2002; 2002WO-IB004132.
 XX
 PR 14-SEP-2001; 2001US-0318994P.
 PR 22-APR-2002; 2002US-0374145P.
 XX
 PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
 PA (MAUR/) MAURER P.
 PA (TISS/) TISSOT A.
 PA (SCHW/) SCHWARZ K.
 PA (MEIJ/) MEIJERINK E.
 PA (LIPO/) LIPOWSKY G.
 PA (PUMP/) PUMPHENS P.
 PA (CIEL/) CIELENS I.
 PA (RENH/) RENHOFA R.
 XX
 PI Maurer P, Tissot A, Schwarz K, Meijerink E, Lipowsky G;
 PI Pumpens P, Cielens I, Renhofa R, Bachmann MF, Storni T;
 XX
 WPI: 2003-354564/33.
 DR
 XX New compositions comprising immunostimulatory substances packaged into virus-like particles, useful as a vaccine for enhancing an immune response in animals, e.g. for treating or preventing allergies, tumors or viral infections.
 PT -
 XX Disclosure; Page 319; 322pp; English.

XX The present invention describes a composition (C) for enhancing an immune
 CC response in an animal. (C) comprises a virus-like particle (VLP), and an
 CC immunostimulatory substance. The immunostimulatory substance is bound to
 CC the VLP. Also described: (1) enhancing an immune response in an animal by
 CC introducing (C) into the animal; (2) producing (C) for enhancing an
 CC immune response in an animal; (3) vaccines comprising (C) together with a
 CC pharmaceutical diluent, carrier or excipient; and (4) immunising or
 CC treating an animal by: (a) administering the vaccine to the animal; (b)
 CC priming a T cell response in the animal by administering the vaccine; or
 CC (c) boosting a T cell response in the animal by administering the
 CC vaccine. (C) has immunostimulant, cytostatic, antiallergic, virucide and
 CC antibacterial activities. (1) can be used in vaccines for enhancing an
 CC immune response in an animal, particularly a mammal or human.
 CC Specifically, (C) is useful for enhancing a B cell response, a T cell
 CC response, or a cytotoxic T-lymphocyte (CTL) response. (C) or a vaccine
 CC comprising (C) can also be used for immunising or treating an animal,
 CC e.g. humans, sheep, horses, cattle, pigs, dogs, cats, rats, birds,
 CC reptiles or fish. (C) is particularly useful in prophylactic or
 CC therapeutic vaccines against allergies, tumours (e.g. breast cancers,
 CC neuroblastoma, or leukaemia), viral diseases (e.g. influenza, hepatitis,
 CC measles or chicken pox), or bacterial infections (e.g. tuberculosis,
 CC pneumonia or syphilis). ACC69790 to ACC69815 and ABR44502 to ABR44612
 CC represent sequences used in the exemplification of the present invention
 XX
 XX Sequence 131 AA;

Query Match 99.1%; Score 660; DB 6; Length 131;
 Best Local Similarity 99.2%; Pred. No. 1.1e-71;
 Matches 130; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MANKTQPTITSTANKIWSDPTRLSTTFSASLLRQKVGI AELNNVSGQYVSVYKRPAP 60
 DB 1 MANKPQPTITSTANKIWSDPTRLSTTFSASLLRQKVGI AELNNVSGQYVSVYKRPAP 60
 QY 61 KPEGCADACVIMPENQSI RTVIGSGAENLATLKAETHKRNVDTLFASGNAGLGLDLP 120
 DB 61 KPEGCADACVIMPENQSI RTVIGSGAENLATLKAETHKRNVDTLFASGNAGLGLDLP 120
 QY 121 TAAIVSSDDTTA 131
 DB 121 TAAIVSSDDTTA 131

RESULT 15
 ADD24202
 ID ADD24202 standard; protein; 131 AA.
 XX
 AC ADD24202;
 XX
 DT 15-JAN-2004 (first entry)
 XX
 DE Bacteriophage AP205 coat protein #1.
 XX
 KW vaccine composition; virus-like particle; core particle;
 KW first attachment site; antigen; antigenic determinant; prion protein;
 KW PrP; PrP peptide; vaccine; neuroprotective; antiinflammatory;
 KW prion disease; Bovine Spongiform Encephalopathy; BSE;
 KW Creutzfeldt-Jakob Disease; prion; AP205; coat protein.
 XX
 OS Bacteriophage AP205.
 XX
 FN WO2003059386-A2.
 XX
 PD 24-JUL-2003.
 XX
 PF 17-JAN-2003; 2003WO-EP000460.
 XX
 PR 18-JAN-2002; 2002US-00050902.
 PR 21-JAN-2002; 2002WO-IB000166.
 PR 08-JUL-2002; 2002US-0393725P.
 PR 18-JUL-2002; 2002US-0396590P.
 XX

PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
 XX
 PI Bachmann M, Maurer P, Pelliccioli E, Renner WA;
 XX
 DR WPI: 2003-598483/56.
 DR N-PSDB; ADD24201.
 XX
 FT A vaccine composition for preventing or treating prion diseases (e.g.
 PT Creutzfeldt-Jakob Disease) comprises a virus-like particle (e.g. RNA-
 PT phage) and at least one prion protein or peptide bound to the virus-like
 PT particle.
 XX
 PS Disclosure; SEQ ID NO 95; 246pp; English.
 XX
 CC This invention relates to a novel vaccine composition comprising a virus-
 CC like or a core particle with at least one first attachment site and at
 CC least one antigen or antigenic determinant that is a prion protein (PrP)
 CC or its dimer, or a PrP peptide, the antigen or antigenic determinant
 CC being bound to the virus-like or core particle. The vaccine of the
 CC invention may have neuroprotective or antiinflammatory activity. The
 CC composition is useful as a medicament or in manufacturing a medicament
 CC for the treatment or prevention of prion diseases. The prion diseases may
 CC include Bovine Spongiform Encephalopathy (BSE) or Creutzfeldt-Jakob
 CC Disease. The present sequence is that of a RNA-phage AP205 coat protein
 CC which is related to the invention.

XX Sequence 131 AA;

Query Match 99.1%; Score 660; DB 7; Length 131;
 Best Local Similarity 99.2%; Pred. No. 1.1e-71;
 Matches 130; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MANKTQPTITSTANKIWSDPTRLSTTFSASLLRQKVGI AELNNVSGQYVSVYKRPAP 60
 DB 1 MANKPQPTITSTANKIWSDPTRLSTTFSASLLRQKVGI AELNNVSGQYVSVYKRPAP 60
 QY 61 KPEGCADACVIMPENQSI RTVIGSGAENLATLKAETHKRNVDTLFASGNAGLGLDLP 120
 DB 61 KPEGCADACVIMPENQSI RTVIGSGAENLATLKAETHKRNVDTLFASGNAGLGLDLP 120
 QY 121 TAAIVSSDDTTA 131
 DB 121 TAAIVSSDDTTA 131

Search completed: June 1, 2005, 09:41:59
 Job time : 114 secs

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OM protein - protein search, using sw model

Run on: June 1, 2005, 09:34:57 ; Search time 24 Seconds
(without alignments)
525.183 Million cell updates/sec

Title: US-10-617-876-1

Perfect score: 668

Sequence: 1 MANKPMQPTSTANKIVWS.....NAGLGFLDPTAIVSSDTTA 131

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR 79:*

2: PIR1:*

3: PIR2:*

4: PIR3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	80	12.0	194	2 S72877	hypothetical prote
2	79	11.8	918	2 A36337	membrane glycoprot
3	78	11.7	305	2 A75334	lacyl-carrier-prot
4	76.5	11.5	546	2 B47073	chaperonin GroEL -
5	75.5	11.3	519	2 I45847	acetylcholine rece
6	73.5	11.0	213	2 D70972	probable enoyl-coA
7	73.5	11.0	291	2 T51668	myb-related transc
8	73.5	11.0	831	2 A11515	ORFA of Listeria s
9	73	10.9	547	2 AC1314	malolactic enzyme
10	72	10.8	273	2 B64446	formylmethanofuran
11	70.5	10.6	414	2 A86229	hypothetical prote
12	70.5	10.6	646	2 T17631	hypothetical prote
13	70.5	10.6	26926	1 I38344	titin, cardiac mus
14	70	10.5	519	2 I56566	nicotinic acetylch
15	70	10.5	519	2 S13874	nicotinic acetylch
16	69.5	10.4	319	2 T27862	hypothetical prote
17	69.5	10.4	358	2 S31407	(2'-5')oligo(A) sy
18	69.5	10.4	643	2 I50539	intermediate filam
19	69.5	10.4	942	1 JQ1674	protein kinase TMK
20	69.5	10.4	1078	2 T30860	trial protein - Sal
21	69	10.3	374	2 T10415	virus envelope pro
22	69	10.3	562	2 S38149	Sis2 protein - yea
23	69	10.3	666	2 S29349	hypothetical prote
24	69	10.3	2187	2 S60224	polyketide synthas
25	68	10.2	252	2 C69172	conserved hypotet
26	68	10.2	267	2 A97762	hypothetical prote
27	68	10.2	350	2 S51494	arabinogalactan en
28	67.5	10.1	330	2 T37854	probable IUNH-fam
29	67.5	10.1	577	2 H69354	probable fatty-aci

30	67.5	10.1	903	2 T09143	alpha-glucosidase
31	67.5	10.1	913	2 AC2445	hypothetical prote
32	67.5	10.1	1052	2 A10346	Acbr/Acrb/Acrf fam
33	67	10.0	143	2 T14664	hypothetical prote
34	67	10.0	220	2 T14951	hypothetical prote
35	67	10.0	398	2 E82262	hypothetical prote
36	67	10.0	454	2 S16522	mitosis-specific c
37	67	10.0	507	2 B84506	probable Athila re
38	67	10.0	701	2 S35313	TiP1 protein - yea
39	67	10.0	772	1 A44052	outer layer protei
40	67	10.0	1056	2 T33167	hypothetical prote
41	67	10.0	1350	2 T30341	zinc finger protei
42	67	10.0	6805	2 S20901	titin - rabbit (fr
43	66.5	10.0	194	2 C86676	hypothetical prote
44	66.5	10.0	419	2 T36272	hypothetical prote
45	66.5	10.0	625	2 C25977	phosphotransferase

ALIGNMENTS

RESULT 1

S72877

hypothetical protein B2126_F3.115 - Mycobacterium leprae

C;Species: Mycobacterium leprae

C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004

C;Accession: S72877

R;Smith, D.R.; Robinson, K.

submitted to the EMBL Data Library, November 1993

A;Description: Mycobacterium leprae cosmid B2126.

A;Reference number: S72585

A;Accession: S72877

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-194 <SMI>

A;Cross-references: UNIPROT:Q49803; EMBL:U00017; NID:g466994; PIDN:AAAL7217.1; PID:g46700

C;Genetics:

A;Start codon: GTG

Query Match 12.0%; Score 80; DB 2; Length 194;

Best Local Similarity 25.0%; Pred. No. 1.1;

Matches 30; Conservative 10; Mismatches 26; Indels 54; Gaps 6;

QY 8 PITSTANKIVWS--DPTRLSTTFESALLRQVRKVGVIAELNNVSGQVSVYK-----RPAP 60

DB 110 PMTFTANNIAWSKNKPSDLATIS-----VNIAQTNN-----SVESFPMEFTFPF 154

QY 61 KEGGCADACVIMPNENQSIPTVIGSAGNLAATLKAETHKRNVDTLFASGNAGLGFLDP 120

DB 155 PQO-----QSQWLSKRTADMLEFGNSS-GLTNP 182

RESULT 2

A36337

membrane glycoprotein gp130 precursor - human

C;Species: Homo sapiens (man)

C;Date: 12-Apr-1991 #sequence_revision 12-Apr-1991 #text_change 09-Jul-2004

C;Accession: A36337

R;Hibi, M.; Murakami, M.; Saito, M.; Hirano, T.; Taga, T.; Kishimoto, T.

Cell 63, 1149-1157, 1990

A;Title: Molecular cloning and expression of an IL-6 signal transducer, gp130.

A;Reference number: A36337; MUID:91084844; PMID:2261637

A;Accession: A36337

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-918 <HIB>

A;Cross-references: UNIPROT:P40189; GB:M57230; NID:g186353; PIDN:AAA59155.1; PID:g186354

C;Genetics:

A;Gene: GDB:IL6ST; GP130

A;Cross-references: GDB:126725; OMIM:600694

A;Map position: 5q11-5q11

C;Keywords: glycoprotein; membrane protein

F;134-316/Domain: cytokine receptor homology <CRS>

Query Match 11.8%; Score 79; DB 2; Length 918;
Best Local Similarity 25.5%; Pred. No. 9.3;
Matches 25; Conservative 21; Mismatches 36; Indels 16; Gaps 5;

QY 9 ITSTANKIVSDPRLSTTFSASLLR-ORVKVGIAELNNVSGQYVYKRPAPKEGCAD 67
DB 82 INRTASSVTFDIASLNLIQTLCNLTFGQLEQNVYGITIISG-----LPPEKPKNL-- 132
QY 68 ACVIMPNENOSIRTVISGSAENLA---TLKAEWETHK 101
DB 133 SCIV--NEGKMKCEWDGGRETHLETNFTLKSEWATHK 168

RESULT 3
A75334
[acyl-carrier-protein] S-malonyltransferase (EC 2.3.1.39) DR1945 [similarity] - Deinococcus
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: A75334
R;White, O.; Eisen, J.A.; Heideberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896; PMID:10567266
A;Accession: A75334
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-305 <WHI>
A;Cross-references: UNIPROT:Q9RT24; GB:AE002033; GB:AE00513; NID:g6459726; PIDN:AAF149
A;Experimental source: strain R1
C;Genetics:
A;Gene: DR1945
A;Map position: 1
C;Superfamily: [acyl-carrier-protein] S-malonyltransferase; [acyl-carrier-protein] S-mal
C;Keywords: acyltransferase; coenzyme A
F;7-286/Domain: [acyl-carrier-protein] S-malonyltransferase homology <AMT>
F;93/Active site: Ser (covalent substrate-binding) #status predicted
F;198/Active site: His #status predicted

Query Match 11.7%; Score 78; DB 2; Length 305;
Best Local Similarity 28.9%; Pred. No. 3.1;
Matches 35; Conservative 14; Mismatches 62; Indels 10; Gaps 4;

QY 13 ANKIVSDPRLSTTFSASLLRQVKVGIAELNNVSGQYVYKRPAPKEGC-ADACVI 71
DB 103 AGVLTLEDAURL-TRKRGELMQQAVPEGVGSAMVMD-----PAVVAEVCQAQGVV 154
QY 72 MP--NENQSIIRTVISGSAENLATLKAETHKRNVDTLFASGNAGLGLDPTAAIVSSDIT 130
DB 155 QPANFNAPQTQTVISGEKAAVDAASAEKTRGLKAIPLKVSAPFHCALMRPAESGLSAELH 214
QY 131 A 131
DB 215 A 215

RESULT 4
B47073
chaperonin GroEL - Chromatium vinosum
C;Species: Chromatium vinosum
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: B47073
R;Ferreyra, R.G.; Soncini, F.C.; Viale, A.M.
J. Bacteriol. 175, 1514-1523, 1993
A;Title: Cloning, characterization, and functional expression in Escherichia coli of cha
A;Reference number: A47073; MUID:93186721; PMID:8444812
A;Accession: B47073
A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-546 <FER>
A;Cross-references: UNIPROT:P31293; GB:M99443; NID:g145007; PIDN:AAA23319.1; PID:g145009

A>Note: sequence extracted from NCBI backbone (NCBIN:126968, NCBI:126970)
C:Superfamily: chaperonin groEL
C;Keywords: molecular chaperone

Query Match 11.5%; Score 76.5; DB 2; Length 546;
Best Local Similarity 20.7%; Pred. No. 8.9;
Matches 28; Conservative 25; Mismatches 65; Indels 17; Gaps 3;

QY 3 NKMPQITSTANKI--VMSDPTLSTTFSASILLRQVRVKGIAELN-----NVS 48
DB 68 NMGAQVKEVASKYSTDIAGDGTATTATVLAQAVMEGLKAVAAGMNPMDLKRGMWDKAVEAA 127
QY 49 GQYVSVYKRPAPKEGGACACVIMPNENQSTRTVISGSAENL---ATLKAETHKRNVD 105
DB 128 TEELKGLSKPCPRPMAIAQVGTISANSDSISCTIIAEAMEKVGKEGVITVEDGTSIQNEL 187
QY 106 TLPASGNAGLGFDP 120
DB 188 DVVEGMQFDRLGTLSP 202

RESULT 5
I45847
acetylcholine receptor - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 15-Oct-1996 #sequence_revision 15-Oct-1996 #text_change 09-Jul-2004
C:Accession: I45847
R:Takai, T.; Noda, M.; Furutani, Y.; Takahashi, H.; Notake, M.; Shimizu, S.; Kayano, T.;
Eur. J. Biochem. 143, 109-115, 1984
A:Title: Primary structure of gamma subunit precursor of calf-muscle acetylcholine receptor
A:Reference number: I45847; MUID:84285374; PMID:6547904
A:Accession: I45847
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-519 <TAK>
A:Cross-references: UNIPROT:P15336; GB:M28307; NID:g162601; PIDN:AAA30351.1; PID:g162602
C:Genetics:
A:Gene: AChR
C:Superfamily: acetylcholine receptor
C;Keywords: neurotransmitter receptor

Query Match 11.3%; Score 75.5; DB 2; Length 519;
Best Local Similarity 22.0%; Pred. No. 11;
Matches 37; Conservative 21; Mismatches 59; Indels 51; Gaps 6;

QY 4 KPMQPI-----TSTANKIVMSDPTLSTTFSASILLRQVRVKGIA-----EL 44
DB 360 RPLAPVAVQDAHPRLONGSSSGNPIPAGEEVALCUPRSELLFRQQRNLGVRAALEKLEK 419
QY 45 NNVSQ---YVSVYKRPAPKEGGACACVIMPNENQSTRTVISGSAENLATLKAETHK 101
DB 420 GPESQSQPEWCGLSKQAAPATQACVEACNLITARAHQHTHFDPSGN-----KEWFLVG 471
QY 102 RNVD-----TLPASGNAGLGF-----DPTAAIVSSD 128
DB 472 RVLDRVCFGLMLSLFVCTAGIFLMAHYNRYVPALPFPDPRSYLPSSD 519

RESULT 6
D70372
probable enoyl-coA hydratase - Mycobacterium tuberculosis (strain H37RV)
C:Species: Mycobacterium tuberculosis
C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 16-Aug-2004
C:Accession: D70372
R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.;
Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.;
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A:Reference number: A70500; MUID:98295987; PMID:9634230
A:Accession: D70372
A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA
A;Residues: 1-213 <COL>
A;Cross-references: UNIPROT:O50402; GB:AL123456; NID:G3242262; PIDN:CAA1579
A;Experimental source: strain H37Rv
C;Genetics:
A;Gene: echA18
C;Superfamily: Naphthoate synthase

Query Match 11.0%; Score 73.5; DB 2; Length 213;
Best Local Similarity 27.6%; Pred. No. 5.8;
Matches 24; Conservative 14; Mismatches 42; Indels 7; Gaps 3;
QY 33 LRORVKVGIALLNNVSGYVSV---YKRPAPKEGCADACVIMPNENQSIQRTVWISGAE 88
Db 1 MRRATWTKMDASNPCCGDIIEAECOLMREOPPAEYVDRVALQRHNRVALITLSHPQAA 60
QY 89 NLATLKAETHKRNVDTLFASGNAGL 115
Db 61 NALNL-ASWRLKRLDLDL--AGESGL 84

RESULT 7
T51668
myb-related transcription factor MYB61 [imported] - Arabidopsis thaliana (fragment)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 09-Jul-2004
C;Accession: T51668
R;Kranz, H.D.; Denekamp, M.; Greco, R.; Jin, H.; Kranz, H.D.; Denekamp, M.; Greco, R.; J
Plant J. 16, 263-276, 1998
A;Title: Towards functional characterisation of the members of the R2R3-MYB gene from Ar
A;Reference number: Z14349; MUID:9839469; PMID:9839469
A;Accession: T51668
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-291 <R>
A;Cross-references: UNIPROT:Q9SBP9; EMBL:AF062896; PIDN:AAC93618.1
A;Experimental source: cultivar Columbia
C;Genetics:
A;Gene: MYB61
A;Map position: 1
C;Keywords: transcription factor

Query Match 11.0%; Score 73.5; DB 2; Length 291;
Best Local Similarity 23.0%; Pred. No. 8.4;
Matches 32; Conservative 19; Mismatches 67; Indels 21; Gaps 5;
QY 3 NKPMQPTITANK--IIVNSDPTRLSTTFSSALLRQVRKVGIAELNNVS-----G 49
Db 76 NDHKSPSSSATNQDFLERPSDLSYFGFKLNFNSLGLSVTTDSSLCSMTIPPQFSPG 135
QY 50 QYV-SVYKRPAPKEGCADACVIMPNENQSIQRTVWISGAEENLATLKAETHKRNVDTLF 108
Db 136 NMVGSVLQTPV-----CVKESISLPHDNNSSSIFSGDHYKLAAPNWFQTNNTNSNFF 190
QY 109 ASGNAGLGLDPTAAIVSS 127
Db 191 --DNCGFSWISPSSTSSS 207

RESULT 8
A11515
ORF of *Listeria seeligeri*, (LPXTG motif) homolog lin0665 [imported] - *Listeria innocua*
C;Species: *Listeria innocua*
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Accession: A11515
R;Glaser, P.; Frangul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussauget, O.; Entian, K.D.; Fsihi, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A;Title: Comparative genomics of *Listeria* species.

A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: A11515
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-831 <GLA>
A;Cross-references: UNIPROT:Q92DZ6; GB:AL592022; PIDN:CAC95897.1; PID:gl6413105; GSPDB:G
A;Experimental source: strain Clp11262
C;Genetics:
A;Gene: lin0665

Query Match 11.0%; Score 73.5; DB 2; Length 831;
Best Local Similarity 25.8%; Pred. No. 30;
Matches 34; Conservative 18; Mismatches 53; Indels 27; Gaps 7;
QY 8 PITSTAN-KIVNSDPTRLSTTFSSALLRQVRKVGIAELNNVSGQ-----YVSVYKRPAP-- 60
Db 646 PLVSDMNDKVGKVGPGDYEVTLNA-----VNEDGVAEAETFFIVRLKSPAPII 694
QY 61 --KPEGCADACVIMPNENQSIQRTVWISGAEENLATL-----KAETHKRNVDTLFASGNA 113
Db 695 TVDPEVSYDSAIL-KNETELLKEVRAKTNDNSAITSADPKVKWQTPGSGYTVTLNAVNE 753
QY 114 GLGLDPTAAIV 125
Db 754 GIP-ADPVTFFIV 764

RESULT 9
AC1314
malolactic enzyme (malate dehydrogenase) homolog lmo1915 [imported] - *Listeria monocytogenes*
C;Species: *Listeria monocytogenes*
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Accession: AC1314
R;Glaser, P.; Frangul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussauget, O.; Entian, K.D.; Fsihi, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A;Title: Comparative genomics of *Listeria* species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AC1314
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-547 <GLA>
A;Cross-references: UNIPROT:Q9Y5Y8; GB:NC_003210; PIDN:CAC9993.1; PID:gl64111368; GSPDB:G
A;Experimental source: strain EGD-e
C;Genetics:
A;Gene: lmo1915
C;Superfamily: malate dehydrogenase (oxaloacetate-decarboxylating)

Query Match 10.9%; Score 73; DB 2; Length 547;
Best Local Similarity 25.0%; Pred. No. 20;
Matches 33; Conservative 21; Mismatches 56; Indels 22; Gaps 4;
QY 12 TANKIVNSDPTRLSTTFSSALLRQVRKVGIAELNNVSGQVSVYKRPAPK-----PEGC 65
Db 191 TNNETLLNDPLYLG-----NKRPLSESYDAFIASFVNVKVEFPAKILLHWEDEGR 242
QY 66 ADACVIMPNENQSIQRTV-----ISGS-----AENLATLKAETHKRNVDTLFASGNAGLGP 117
Db 243 ANASRILNHYRDKICTFNDDIQGTGMVVAVALTIQVSRIPLSSEQKIIFGAGTAGIGI 302
QY 118 LDPTAAIVSSDT 129
Db 303 ADQLSAQLMRET 314

RESULT 10
B64446
formylmethanofuran dehydrogenase (EC 1.2.99.5) (tungsten) chain C - *Methanococcus jannaschii*
C;Species: *Methanococcus jannaschii*
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 16-Aug-2004

```
C|Accession: B64446  
R|Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake,  
A.; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.  
rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.  
Science 273, 1058-1073, 1996  
A|Authors: Kane, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.  
A|Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii  
A|Reference number: A64300; UID:96337999; PMID:8688087  
A|Accession: B64446  
A|Status: preliminary; nucleic acid sequence not shown; translation not shown  
A|Molecule type: DNA  
A|Residues: 1-273 <BUL>  
A|Cross-references: UNIPROT.Q58571; GB.U67558; GB.L77117; NID:g1591786; PIDN:AAB99173.1-  
C|Genetics:  
A|Map position: FORL10572-1111393  
C|Superfamily: Formylmethanofuran dehydrogenase, subunit C  
C|Keywords: iron-sulfur protein; metalloprotein; oxidoreductase; tungsten
```

	Query Match	10.8%;	Score 72;	DB 2;	Length 273;	
	Best Local Similarity	27.6%;	Pred. No. 11;	Mismatches	27;	Conservative 14;
						Gaps 4;
Qy	34	RQRVKVG---IAELNNVSGQYVVYKPAKP-----PEGCADACVMPNEN	76			
	::	:::::	:	: ::	:	:
Dd	43	KRKIKVADIFDVELNDIEGSPRIKVNSPKLYIGSKMTKGIVVEG--DAGMYVGAEM	100			
	::	:::::	:	: ::	:	:
Qy	77	QSRTVTWISGAENLATLKAEWETHKRNVDTLFASGNAG	114			
	::	:::::	:	: ::	:	:
Dd	101	KGGKIVVNGNAES-----WAGONMKGGELLTKGNAG	131			
	::	:::::	:	: ::	:	:

RESULT 11

A86229

hypothetical protein [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004

C:Accession: A86229

Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Jensen, N.F.; Hughes, B.; Huizlar, L.

Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; MUID:21016719; PMID:11130712

A:Accession: A86229

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-414 <STO>

A:Cross-references: UNIPROT:Q9SAV9; GB:AE005172; NID:g3482929; PIDN:AAC33214.1; GSPDB:GN

C:Genetics:

A:Map position: 1

C:Superfamily: petunia myb-related protein 1; myb DNA-binding repeat homology

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Query Match      10.6%; Score 70.5; DB 2; Length 414;
Best Local Similarity 23.0%; Pred. No. 26;
Matches 32; Conservative 18; Mismatches 68; Indels 21; Gaps 5;

Qy      3  NKMPQITSTANK--IWSDPTLSTTFSASLLRQVRKVGIAELNNVS-----G 49
          |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db      151 NDHKSPSSSATNQDFLERPSDLSDYFGQKLNFSNLGLSVTTDSSLCMIPPQFSPG 210
          |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Qy      50  QYV-SVYKRAPKEGCADCVIMPNENQISRTVIGSSAENLATLKAETHKRVDTLF 108
          |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db      211 NMVGSVLQTPV-----CVKPSISLIPDPNNSSPSIGGDHVKLAAPNWEFQTNNNNTSNFF 265
          |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Qy      109 ASGNAGLGFLDPTAAIVSS 127
          |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db      266 --DNGGFSWSIPNSSTSS 282
          |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |

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RESULT 12
Ti7631
hypothetical protein A140R - Chlorella virus PBCV-1
C:Species: Chlorella virus PBCV-1
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: Ti7631
R:Graves, M.V.; Van Etten, J.L.
submitted to the EMBL Data Library, May 1999
A:Reference number: Z18806
A:Accession: Ti7631
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-846 <GRA>
A:Cross-references: UNIPROT.Q84460; EMBL.U42580; NID:G4028896; PIDN:AAC96508.1
A:Experimental source: specific host Chlorella strain NC64A
C:Genetics:
A>Note: A140R

Query Match      10.6%; Score 70.5; DB 2; Length 646;
Best Local Similarity 24.8%; Pred. No. 45;
Matches    26; Conservative   15; Mismatches   33; Indels    31; Gaps     S

QY      4 KPMOPI-----TSTANKI--VMSDDPTLSITFSASILLRRVKVG---IAELNN 46
          |||:         |||:        :||:       :|||:       |
Db      500 KTPAVGTIIITAAKVTAPVNANKVSLOYTEKNKKLTKVTVTKTHGMKVGAEVDVVVRNK 559
          |||:         |||:        :||:       :|||:       |

QY      47 VSGQYVSVYK----RPAPKPGE-----CADACVIMPNEHQ 77
          :|||:         :|||:        :|||:       :|||:       |
Db      560 DPYAFVAIVYYKGAIKPPAKPAGKPTAPAGTTIVIAAKVTAVPNTNK 604
          :|||:         :|||:        :|||:       :|||:       |

```

RESULT 13

138344

titin, cardiac muscle [validated] - human

N;Alternate names: connectin

N;Contains: serine/threonine-specific protein kinase (EC 2.7.1.1--)

C;Species: Homo sapiens (man)

C;Date: 12-Aug-1996 #sequence revision 12-Aug-1996 #text change 09-Jul-2004

C;Accession: I38344; I38345; S20898; S20897; S20899; S63665; S37393

R;Labelit, S.; Kolmerer, B.

R;Science 270, 293-296, 1995

A;Title: Titins: giant proteins in charge of muscle ultrastructure and elasticity

A;Reference number: A57430; MUID:96026330; PMID:7569978

A;Accession: I38344

A;Status: nucleic acid sequence not shown; translation not shown; translated for

A;Molecule type: mRNA

A;Residues: 1-26926 <LAB1>

A;Cross-references: UNIPROT:Q10466; EMBL:X90568; NID:gi017424; PID:gi017425

R;Musco, G.; Triatzios, C.; Schuck, P.; Pastore, A.

R;Biochemistry 34, 553-561, 1995

A;Title: Dissecting titin into its structural motifs: identification of an alpha

A;Reference number: I38345; MUID:95119041; PMID:7819249

A;Accession: I38345

A;Status: nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1977-2014 <MUS>

A;Cross-references: EMBL:X83270; NID:9602579; PIDN:CAAS8243.1; PID:9602580

A;Note: Conformation and properties are reported for a synthetic peptide corre

R;Labelit, S.; Gautel, M.; Lakey, A.; Trinick, J.

R;EMBO J. 11, 1711-1716, 1992

A;Title: Towards a molecular understanding of titin.

A;Reference number: S20897; MUID:92259380; PMID:1582406

A;Accession: S20898

A;Status: nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 13597-14200, 'I', 14202-14696 <LAB2>

A;Cross-references: EMBL:X64698; NID:G37192; PIDN:CAA45939.1; PID:G37193

A;Accession: S20897

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: mRNA

A;Residues: 16330-16382, 'S', 16384-16756, 'F', 16758-16860 <LAB3>

A;Cross-references: EMBL:X64699; NID:G37190; PIDN:CAA45940.1; PID:G37191

A;Accession: I56566
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-519 <RES>
A;Cross-references: UNIPROT:P04760; GB:M30514; NID:g200013
R;Yu, L.; LaPolla, R.J.; Davidson, N.
Nucleic Acids Res. 14, 3539-3555, 1986
A;Title: Mouse muscle nicotinic acetylcholine receptor gamma-subunit: cDNA sequence and
A;Reference number: A24919; MUID:86205253; PMID:3010242
A;Accession: A24919
A;Molecule type: mRNA
A;Residues: 1-230, 'V', 232-345, 'L', 347-519, 'X' <YUL>
A;Note: the authors translated the codon ATG for residue 116 as His
R;Gardner, P.D.; Heinemann, S.; Patrick, J.
Brain Res. Mol. Brain Res. 3, 69-76, 1987
A;Title: Transcriptional regulation of nicotinic acetylcholine receptor genes: identifier
A;Reference number: A43774
A;Accession: A43774
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-57 <GAR>
A;Cross-references: GB:M27455; NID:g387692; PIDN:AAA70247.1; PID:g191613
R;Crowder, C.M.; Merlie, J.P.
Mol. Cell. Biol. 8, 5257-5267, 1988
A;Title: Stepwise activation of the mouse acetylcholine receptor delta- and gamma-subun
A;Reference number: 149457; MUID:89218986; PMID:3244354
A;Accession: 149457
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-18 <RE2>
A;Cross-references: GB:M22381; NID:g191597; PIDN:AAA37152.1; PID:g553854
C;Genetics:
A;Note: list of introns may be incomplete
C;Superfamily: acetylcholine receptor
C;Keywords: glycoprotein; ion channel; neurotransmitter receptor; postsynaptic membrane;
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-519/Product: nicotinic acetylcholine receptor gamma chain #status predicted <MAT>

Query Match 10.5%; Score 70; DB 2; Length 519;
Best Local Similarity 25.7%; Pred. No. 38;
Matches 27; Conservative 14; Mismatches 38; Indels 26; Gaps 4;

Qy . 29 SASLLRQRVKVGIAE-----LN-----VSQQYSVYKRPAPKPGCADACVIMPNENQS 78
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397 SEILFRQRRGLVOAVLEKLENGPEVRQSEFCGSLKQASPAIQACVDACNLMARARRQ 456

Qy 79 IRTVISSAENLATLKAEWETHKNVD-----TLFASGNAGL 115
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457 QSHFDSDGN-----EWLLVGRVLDRVCFLAMLSLFCGTAGI 493

RESULT 15
SI3874
nicotinic acetylcholine receptor gamma chain precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: SI3874; S03082
R;Witzemann, V.; Stein, E.; Barg, B.; Konno, T.; Koenen, M.; Kues, W.; Criado, M.; Hofmar
Eur. J. Biochem. 194, 437-448, 1990
A;Title: Primary structure and functional expression of the alpha-, beta-, gamma-, delta
A;Reference number: SI3872; MUID:91099317; PMID:1702709
A;Accession: SI3874
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-519 <WIT>
A;Cross-references: UNIPROT:P18916; EMBL:X74934; NID:g398835; PIDN:CAA52828.1; PID:g39886;
R;Witzemann, V.; Barg, B.; Nishikawa, Y.; Sakmann, B.; Numa, S.
FEBS Lett. 223, 104-112, 1987
A;Title: Differential regulation of muscle acetylcholine receptor gamma- and epsilon-subu
A;Reference number: S03081; MUID:88030021; PMID:3666131
A;Accession: S03082
A;Molecule type: DNA

A;Residues: 203-306 <W12>
A;Cross-references: EMBL:X06364; NID:G55588; PIDN:CAA29662.1; PID:G55589
C;Superfamily: acetylcholine receptor
C;Keywords: Glycoprotein; ion channel; neurotransmitter receptor; postsynaptic membrane;
E;39-65/Domain: transmembrane #status predicted <TM1>
F;72-90/Domain: transmembrane #status predicted <TM2>

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Best Local Similarity	25.8%;	Pred. No. 38;		
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Qy	64	GCADACVIMPNENQSIPTVIGSAENLATLKAWEIHKRNVD-----	TLFASGNAGL 115	
Db	442	ACVDACNLMARHQSHFDSGN-----	EWLLVGRVLDRCVFLAMLSLFCGTAGI 493	

Search completed: June 1, 2005, 09:46:47
Job time : 26 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 1, 2005, 09:38:08 ; Search time 91 Seconds
(without alignments)
497.627 Million cell updates/sec

Title: US-10-617-876-1

Perfect score: 668

Sequence: 1 MANKMPQITSTANKIWSDPTRLSLTFSSASLRQRVKVGAELNNVSGQVSVYKRPAP 131

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1465611 seqs, 345679903 residues

Total number of hits satisfying chosen parameters: 1465611

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications AA:*
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2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
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15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep:*
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18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	668	100.0	131	14	US-10-243-739-80
2	668	100.0	131	14	US-10-244-065-80
3	668	100.0	131	14	US-10-289-454-80
4	668	100.0	131	15	US-10-346-190-95
5	668	100.0	131	15	US-10-465-811-90
6	668	100.0	131	15	US-10-289-456-112
7	668	100.0	131	15	US-10-622-064-14
8	668	100.0	131	15	US-10-617-876-1
9	668	100.0	131	15	US-10-622-124-28
10	668	100.0	131	16	US-10-622-087-28
11	660	98.8	131	14	US-10-243-739-81
12	660	98.8	131	14	US-10-244-065-81
13	660	98.8	131	14	US-10-289-454-81

14	660	98.8	131	15	US-10-346-190-96	Sequence 96, Appl
15	660	98.8	131	15	US-10-465-811-93	Sequence 93, Appl
16	660	98.8	131	15	US-10-289-456-113	Sequence 113, Appl
17	660	98.8	131	15	US-10-622-064-18	Sequence 18, Appl
18	660	98.8	131	15	US-10-617-876-3	Sequence 3, Appl
19	660	98.8	131	15	US-10-622-124-29	Sequence 29, Appl
20	660	98.8	131	16	US-10-622-087-29	Sequence 29, Appl
21	83.5	12.5	1619	16	US-10-437-963-121378	Sequence 121378,
22	81.5	12.2	662	16	US-10-437-963-121381	Sequence 121381,
23	81.5	12.2	1163	16	US-10-437-963-121376	Sequence 121376,
24	80	12.0	194	14	US-10-080-170-161	Sequence 161, App
25	80	12.0	194	16	US-10-080-170-161	Sequence 161, App
26	80	12.0	194	16	US-10-468-356-161	Sequence 161, App
27	79	11.8	329	16	US-10-755-883-426	Sequence 426, App
28	79	11.8	332	9	US-09-313-942-10	Sequence 10, Appl
29	79	11.8	332	9	US-09-935-868-10	Sequence 10, Appl
30	79	11.8	332	14	US-10-287-035-10	Sequence 10, Appl
31	79	11.8	332	14	US-10-282-162-10	Sequence 2, Appl
32	79	11.8	488	13	US-10-079-625-5	Sequence 5, Appl
33	79	11.8	708	14	US-10-313-135-2	Sequence 12, Appl
34	79	11.8	807	15	US-10-311-473-12	Sequence 7, Appl
35	79	11.8	859	9	US-09-313-942-7	Sequence 7, Appl
36	79	11.8	859	9	US-09-935-868-7	Sequence 7, Appl
37	79	11.8	859	14	US-10-287-035-7	Sequence 7, Appl
38	79	11.8	859	14	US-10-282-162-7	Sequence 7, Appl
39	79	11.8	918	10	US-09-853-180-4	Sequence 4, Appl
40	79	11.8	918	10	US-09-972-708-8	Sequence 8, Appl
41	79	11.8	918	14	US-10-177-293-230	Sequence 230, App
42	79	11.8	918	15	US-10-295-027-74	Sequence 74, Appl
43	79	11.8	918	15	US-10-058-270A-32	Sequence 32, Appl
44	79	11.8	918	16	US-10-715-667-8	Sequence 8, Appl
45	79	11.8	918	17	US-10-850-270-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1

US-10-243-739-80
; Sequence 80, Application US/10243739
; Publication No. US20030091593A1
; GENERAL INFORMATION:
; APPLICANT: Bachmann, Martin F.
; APPLICANT: Storni, Tazio
; APPLICANT: Lechner, Franziska
; TITLE OF INVENTION: In vivo Activation of Antigen Presenting Cells for Enhancement of
; FILE OF INVENTION: Immune Responses Induced by Virus Like Particles
; FILE REFERENCE: 1700.0210001
; CURRENT APPLICATION NUMBER: US/10/243,739
; PRIOR FILING DATE: 2002-09-16
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 80
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: AP205 coat protein
US-10-243-739-80

Query Match	100.0%	Score 668;	DB 14;	Length 131;
Best Local Similarity	100.0%	Pred. No. 7.9e-71;	Mismatches 0;	Indels 0;
Matches 131;	Conservative 0;			
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Db	1	MANKMPQITSTANKIWSDPTRLSLTFSSASLRQRVKVGAELNNVSGQVSVYKRPAP	60	
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QY      121 TAAIVSSDTTA 131
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Db      121 TAAIVSSDTTA 131

RESULT 2
US-10-244-065-80
; Sequence 80, Application US/10244065
; Publication No. US20030099668A1
; GENERAL INFORMATION:
; APPLICANT: Bachmann, Martin F.
; APPLICANT: Storni, Tazio
; APPLICANT: Maurer, Patrick
; APPLICANT: Tissot, Alain
; APPLICANT: Schwarz, Katrin
; APPLICANT: Meijerink, Edwin
; APPLICANT: Lipowski, Gerard
; APPLICANT: Pumps, Paul
; APPLICANT: Cielens, Indulis
; APPLICANT: Renhofs, Regina
; TITLE OF INVENTION: Packaging of Immunostimulatory Substances into Virus-like Particles
; TITLE OF INVENTION: Method of Preparation and Use
; FILE REFERENCE: 1700.0220001
; CURRENT APPLICATION NUMBER: US/10/244,065
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 60/374,145
; PRIOR FILING DATE: 2002-04-22
; PRIOR APPLICATION NUMBER: 60/318,994
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 80
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: AP205 coat protein
US-10-244-065-80

Query Match      100.0%; Score 668; DB 14; Length 131;
Best Local Similarity 100.0%; Pred. No. 7.9e-71;
Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MANKPMQPIITSTANKIIVSDPTLSTTFSASLLRQKVKVGLAEINNVSGQYVSVYKRPAP 60
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QY      61 KPEGCADACVIMPNENQSIPTVSSAENLATLKAETHKRNVDTLFASGNAGLGLDLP 120
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QY      121 TAAIVSSDTTA 131
      |||||
Db      121 TAAIVSSDTTA 131

RESULT 3
US-10-289-454-80
; Sequence 80, Application US/10289454
; Publication No. US20030157479A1
; GENERAL INFORMATION:
; APPLICANT: Bachmann, Martin
; APPLICANT: Jennings, Gary
; APPLICANT: Sonderegger, Ivo
; TITLE OF INVENTION: Antigen Arrays for Treatments of Allergic Eosinophilic Diseases
; FILE REFERENCE: 1700.0360001
; CURRENT APPLICATION NUMBER: US/10/289,454
; CURRENT FILING DATE: 2003-02-10
; PRIOR APPLICATION NUMBER: US 60/396,636
; PRIOR FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: PCT/IB02/00166
; PRIOR FILING DATE: 2002-01-21
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; PRIOR APPLICATION NUMBER: US 10/050,902
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/331,045
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 386
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 80
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: AP205 coat protein
US-10-289-454-80

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Best Local Similarity 100.0%; Pred. No. 7.9e-71;
Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      1 MANKPMQPIITSTANKIIVSDPTLSTTFSASLLRQKVKVGLAEINNVSGQYVSVYKRPAP 60

QY      61 KPEGCADACVIMPNENQSIPTVSSAENLATLKAETHKRNVDTLFASGNAGLGLDLP 120
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Db      61 KPEGCADACVIMPNENQSIPTVSSAENLATLKAETHKRNVDTLFASGNAGLGLDLP 120

QY      121 TAAIVSSDTTA 131
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Db      121 TAAIVSSDTTA 131

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US-10-346-190-95
; Sequence 95, Application US/10346190
; Publication No. US20030219459A1
; GENERAL INFORMATION:
; APPLICANT: Bachmann, Martin
; APPLICANT: Maurer, Patrick
; APPLICANT: Pelliccioli, Erica
; APPLICANT: Renner, Wolfgang A.
; TITLE OF INVENTION: Prion Protein Carrier-Conjugates
; FILE REFERENCE: 1700.0290003
; CURRENT APPLICATION NUMBER: US/10/346,190
; CURRENT FILING DATE: 2003-01-17
; PRIOR APPLICATION NUMBER: 60/396,590
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/393,725
; PRIOR FILING DATE: 2002-07-08
; PRIOR APPLICATION NUMBER: 60/389,898
; PRIOR FILING DATE: 2002-06-20
; PRIOR APPLICATION NUMBER: PCT/IB02/00166
; PRIOR FILING DATE: 2002-01-21
; PRIOR APPLICATION NUMBER: 10/050,902
; PRIOR FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 164
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 95
; LENGTH: 131
; TYPE: PRT
; ORGANISM: RNA-phage AP205
US-10-346-190-95

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Best Local Similarity 100.0%; Pred. No. 7.9e-71;
Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MANKPMQPIITSTANKIIVSDPTLSTTFSASLLRQKVKVGLAEINNVSGQYVSVYKRPAP 60
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Db      1 MANKPMQPIITSTANKIIVSDPTLSTTFSASLLRQKVKVGLAEINNVSGQYVSVYKRPAP 60

QY      61 KPEGCADACVIMPNENQSIPTVSSAENLATLKAETHKRNVDTLFASGNAGLGLDLP 120
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Db      61 KPEGCADACVIMPNENQSIPTVSSAENLATLKAETHKRNVDTLFASGNAGLGLDLP 120
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QY 121 TAAIVSSDTTA 131
Db 121 TAAIVSSDTTA 131

RESULT 5
US-10-465-811-90
; Sequence 90, Application US/10465811
; Publication No. US2004005338A1
; GENERAL INFORMATION:
; APPLICANT: BACHMANN, MARTIN F
; APPLICANT: RENNER, WOLFGANG A
; TITLE OF INVENTION: PACKAGED VIRUS-LIKE PARTICLES FOR USE AS ADJUVANTS:
; FILE REFERENCE: 1700.0290004
; CURRENT APPLICATION NUMBER: US/10/465,811
; CURRENT FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: US 60/389,898
; PRIOR FILING DATE: 2002-06-20
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 90
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Bacteriophage AP205
US-10-465-811-90

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Best Local Similarity 100.0%; Pred. No. 7.9e-71;
Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 KPEGCADACVIMPNENQSI RTVSSGAENLATLKAETHKRNVDTLFASGNAGLGLDLP 120
Db 61 KPEGCADACVIMPNENQSI RTVSSGAENLATLKAETHKRNVDTLFASGNAGLGLDLP 120

QY 121 TAAIVSSDTTA 131
Db 121 TAAIVSSDTTA 131

RESULT 6
US-10-289-456-112
; Sequence 112, Application US/10289456
; Publication No. US20040033211A1
; GENERAL INFORMATION:
; APPLICANT: Bachmann, Martin
; APPLICANT: Maurer, Patrick
; APPLICANT: Spohn, Gunther
; TITLE OF INVENTION: Antigen Arrays for Treatment of Bone Disease
; FILE REFERENCE: 1700.0330001
; CURRENT APPLICATION NUMBER: US/10/289,456
; CURRENT FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: PCT/IB02/00166
; PRIOR FILING DATE: 2002-01-21
; PRIOR APPLICATION NUMBER: US 10/050,902
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/396,635
; PRIOR FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: US 60/331,045
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 112
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: AP205 coat protein

Query Match 100.0%; Score 668; DB 15; Length 131;
Best Local Similarity 100.0%; Pred. No. 7.9e-71;
Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MANKPMQPISTANKIWSDPTRLSTTFSASLLRQKVKVGI AELNNVSGQYVSVYKRPAP 60
Db 1 MANKPMQPISTANKIWSDPTRLSTTFSASLLRQKVKVGI AELNNVSGQYVSVYKRPAP 60

QY 61 KPEGCADACVIMPNENQSI RTVSSGAENLATLKAETHKRNVDTLFASGNAGLGLDLP 120
Db 61 KPEGCADACVIMPNENQSI RTVSSGAENLATLKAETHKRNVDTLFASGNAGLGLDLP 120

QY 121 TAAIVSSDTTA 131
Db 121 TAAIVSSDTTA 131
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US-10-289-456-112

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Query Match 100.0%; Score 668; DB 15; Length 131;
Best Local Similarity 100.0%; Pred. No. 7.9e-71;
Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MANKPMQPISTANKIWSDPTRLSTTFSASLLRQKVKVGI AELNNVSGQYVSVYKRPAP 60
Db 1 MANKPMQPISTANKIWSDPTRLSTTFSASLLRQKVKVGI AELNNVSGQYVSVYKRPAP 60

QY 61 KPEGCADACVIMPNENQSI RTVSSGAENLATLKAETHKRNVDTLFASGNAGLGLDLP 120
Db 61 KPEGCADACVIMPNENQSI RTVSSGAENLATLKAETHKRNVDTLFASGNAGLGLDLP 120

QY 121 TAAIVSSDTTA 131
Db 121 TAAIVSSDTTA 131
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RESULT 7

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US-10-622-064-14
; Sequence 14, Application US/10622064
; Publication No. US20040059094A1
; GENERAL INFORMATION:
; APPLICANT: Bachmann, Martin F
; APPLICANT: Maurer, Patrick F
; TITLE OF INVENTION: Hapten-Carrier Conjugates and Uses Thereof
; FILE REFERENCE: 1700.0300001
; CURRENT APPLICATION NUMBER: US/10/622,064
; CURRENT FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: US 60/396,575
; PRIOR FILING DATE: 2002-07-18
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Bacteriophage AP205
US-10-622-064-14
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Query Match 100.0%; Score 668; DB 15; Length 131;
Best Local Similarity 100.0%; Pred. No. 7.9e-71;
Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MANKPMQPISTANKIWSDPTRLSTTFSASLLRQKVKVGI AELNNVSGQYVSVYKRPAP 60
Db 1 MANKPMQPISTANKIWSDPTRLSTTFSASLLRQKVKVGI AELNNVSGQYVSVYKRPAP 60

QY 61 KPEGCADACVIMPNENQSI RTVSSGAENLATLKAETHKRNVDTLFASGNAGLGLDLP 120
Db 61 KPEGCADACVIMPNENQSI RTVSSGAENLATLKAETHKRNVDTLFASGNAGLGLDLP 120

QY 121 TAAIVSSDTTA 131
Db 121 TAAIVSSDTTA 131
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RESULT 8

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US-10-617-876-1
; Sequence 1, Application US/10617876
; Publication No. US20040076611A1
; GENERAL INFORMATION:
; APPLICANT: Bachmann, Martin F
; APPLICANT: Tisseot, Alain
; APPLICANT: Pumps, Paul
; APPLICANT: Cielens, Indulis
; APPLICANT: Renhofa, Regina
; TITLE OF INVENTION: Molecular Antigen Arrays
; FILE REFERENCE: 1700.0310001
; CURRENT APPLICATION NUMBER: US/10/617,876
; CURRENT FILING DATE: 2003-07-14
; PRIOR APPLICATION NUMBER: US 60/396,126
; PRIOR FILING DATE: 2002-07-17
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; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Bacteriophage AP205
US-10-617-876-1

Query Match      100.0%; Score 668; DB 15; Length 131;
Best Local Similarity 100.0%; Pred. No. 7.9e-71;
Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MANKPMQPISTANKIIVMSDPTRLSTTFSSASLLRQVRKVGIAELNNVSGQYVSVYKRPAP 60
Db 1 MANKPMQPISTANKIIVMSDPTRLSTTFSSASLLRQVRKVGIAELNNVSGQYVSVYKRPAP 60

Qy 61 KPEGCADACVIMPNENQSIQRTVSSAENLATLKAETHKRNVDTLFASGNAGLGLDLP 120
Db 61 KPEGCADACVIMPNENQSIQRTVSSAENLATLKAETHKRNVDTLFASGNAGLGLDLP 120

Qy 121 TAAIVSSDTTA 131
Db 121 TAAIVSSDTTA 131

RESULT 9
US-10-622-124-28
; Sequence 28, Application US/10622124
; Publication No. US20040076645A1
; GENERAL INFORMATION:
; APPLICANT: Bachmann, Martin F
; APPLICANT: Fulurija, Alma
; TITLE OF INVENTION: Ghrelin-Carrier Conjugates
; FILE REFERENCE: 1700.0340001
; CURRENT APPLICATION NUMBER: US/10/622,124
; PRIOR FILING DATE: 2003-07-18
; PRIOR FILING DATE: 2002-07-19
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 28
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Bacteriophage AP205
US-10-622-124-28

Query Match      100.0%; Score 668; DB 15; Length 131;
Best Local Similarity 100.0%; Pred. No. 7.9e-71;
Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MANKPMQPISTANKIIVMSDPTRLSTTFSSASLLRQVRKVGIAELNNVSGQYVSVYKRPAP 60
Db 1 MANKPMQPISTANKIIVMSDPTRLSTTFSSASLLRQVRKVGIAELNNVSGQYVSVYKRPAP 60

Qy 61 KPEGCADACVIMPNENQSIQRTVSSAENLATLKAETHKRNVDTLFASGNAGLGLDLP 120
Db 61 KPEGCADACVIMPNENQSIQRTVSSAENLATLKAETHKRNVDTLFASGNAGLGLDLP 120

Qy 121 TAAIVSSDTTA 131
Db 121 TAAIVSSDTTA 131

RESULT 10
US-10-622-087-28
; Sequence 28, Application US/10622087
; Publication No. US20040141984A1
; GENERAL INFORMATION:
; APPLICANT: Bachmann, Martin F
; APPLICANT: Tissot, Alain
; APPLICANT: Ortman, Rainer
; APPLICANT: Luond, Rainer
; APPLICANT: Staufenbiel, Matthias
```

```
; APPLICANT: Frey, Peter
; TITLE OF INVENTION: Amyloid Beta 1-6 Antigen Arrays
; FILE REFERENCE: 1700.0350002
; CURRENT APPLICATION NUMBER: US/10/622,087
; CURRENT FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: US 60/396,639
; PRIOR FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: US 60/470,432
; PRIOR FILING DATE: 2003-05-15
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 28
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Bacteriophage AP205
US-10-622-087-28

Query Match      100.0%; Score 668; DB 16; Length 131;
Best Local Similarity 100.0%; Pred. No. 7.9e-71;
Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MANKPMQPISTANKIIVMSDPTRLSTTFSSASLLRQVRKVGIAELNNVSGQYVSVYKRPAP 60
Db 1 MANKPMQPISTANKIIVMSDPTRLSTTFSSASLLRQVRKVGIAELNNVSGQYVSVYKRPAP 60

Qy 61 KPEGCADACVIMPNENQSIQRTVSSAENLATLKAETHKRNVDTLFASGNAGLGLDLP 120
Db 61 KPEGCADACVIMPNENQSIQRTVSSAENLATLKAETHKRNVDTLFASGNAGLGLDLP 120

Qy 121 TAAIVSSDTTA 131
Db 121 TAAIVSSDTTA 131

RESULT 11
US-10-243-739-81
; Sequence 81, Application US/10243739
; Publication No. US20030091593A1
; GENERAL INFORMATION:
; APPLICANT: Bachmann, Martin F.
; APPLICANT: Storni, Tazio
; APPLICANT: Lechner, Franziska
; TITLE OF INVENTION: In vivo Activation of Antigen Presenting Cells for Enhancement of
; TITLE OF INVENTION: Immune Responses Induced by Virus Like Particles
; FILE REFERENCE: 1700.0210001
; CURRENT APPLICATION NUMBER: US/10/243,739
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 60/318,967
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 81
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: AP205 coat protein
US-10-243-739-81

Query Match      98.8%; Score 660; DB 14; Length 131;
Best Local Similarity 99.2%; Pred. No. 7e-70;
Matches 130; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MANKPMQPISTANKIIVMSDPTRLSTTFSSASLLRQVRKVGIAELNNVSGQYVSVYKRPAP 60
Db 1 MANKPMQPISTANKIIVMSDPTRLSTTFSSASLLRQVRKVGIAELNNVSGQYVSVYKRPAP 60

Qy 61 KPEGCADACVIMPNENQSIQRTVSSAENLATLKAETHKRNVDTLFASGNAGLGLDLP 120
Db 61 KPEGCADACVIMPNENQSIQRTVSSAENLATLKAETHKRNVDTLFASGNAGLGLDLP 120

Qy 121 TAAIVSSDTTA 131
Db 121 TAAIVSSDTTA 131
```

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Db      121 TAAIVSSDTTA 131

RESULT 12
US-10-244-065-81
; Sequence 81, Application US/10244065
; Publication No. US2003009968A1
; GENERAL INFORMATION:
; APPLICANT: Bachmann, Martin F.
; APPLICANT: Storni, Tazio
; APPLICANT: Maurer, Patrick
; APPLICANT: Tissot, Alain
; APPLICANT: Schwarz, Katrin
; APPLICANT: Meijerink, Edwin
; APPLICANT: Lipowsky, Gerard
; APPLICANT: Pumps, Paul
; APPLICANT: Cielens, Indulis
; APPLICANT: Renhofa, Regina
; TITLE OF INVENTION: Packaging of Immunostimulatory Substances into Virus-like Particles
; TITLE OF INVENTION: Method of Preparation and Use
; FILE REFERENCE: 1700.0220001
; CURRENT APPLICATION NUMBER: US/10/244,065
; PRIOR FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 60/374,145
; PRIOR FILING DATE: 2002-04-22
; PRIOR APPLICATION NUMBER: 60/318,994
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 81
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: AP205 coat protein
US-10-244-065-81

Query Match      98.8%; Score 660; DB 14; Length 131;
Best Local Similarity 99.2%; Pred. No. 7e-70;
Matches 130; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 MANKMPQITSTANKIWSDPTRLSTTFSASLLRQVRKVGVIAELNNVSGQYVSVKRPAP 60
Db      1 MANKTQPISTANKIWSDPTRLSTTFSASLLRQVRKVGVIAELNNVSGQYVSVKRPAP 60

QY      61 KPEGCADACVIMPNENQSIPTVSGSAENLATLKAETHKRNVDTLFASGNAGLGLDLP 120
Db      61 KPEGCADACVIMPNENQSIPTVSGSAENLATLKAETHKRNVDTLFASGNAGLGLDLP 120

QY      121 TAAIVSSDTTA 131
Db      121 TAAIVSSDTTA 131

RESULT 13
US-10-289-454-81
; Sequence 81, Application US/10289454
; Publication No. US20030157479A1
; GENERAL INFORMATION:
; APPLICANT: Bachmann, Martin
; APPLICANT: Jennings, Gary
; APPLICANT: Sonderegger, Ivo
; TITLE OF INVENTION: Antigen Arrays for Treatments of Allergic Eosinophilic Diseases
; FILE REFERENCE: 1700.0360001
; CURRENT APPLICATION NUMBER: US/10/289,454
; PRIOR FILING DATE: 2003-02-10
; PRIOR APPLICATION NUMBER: US 60/396,636
; PRIOR FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: PCT/IB02/00166
; PRIOR FILING DATE: 2002-01-21
; PRIOR APPLICATION NUMBER: US 10/050,902
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/331,045
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; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 386
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 81
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: AP205 coat protein
US-10-289-454-81

Query Match      98.8%; Score 660; DB 14; Length 131;
Best Local Similarity 99.2%; Pred. No. 7e-70;
Matches 130; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 MANKMPQITSTANKIWSDPTRLSTTFSASLLRQVRKVGVIAELNNVSGQYVSVKRPAP 60
Db      1 MANKTQPISTANKIWSDPTRLSTTFSASLLRQVRKVGVIAELNNVSGQYVSVKRPAP 60

QY      61 KPEGCADACVIMPNENQSIPTVSGSAENLATLKAETHKRNVDTLFASGNAGLGLDLP 120
Db      61 KPEGCADACVIMPNENQSIPTVSGSAENLATLKAETHKRNVDTLFASGNAGLGLDLP 120

QY      121 TAAIVSSDTTA 131
Db      121 TAAIVSSDTTA 131

RESULT 14
US-10-346-190-96
; Sequence 96, Application US/10346190
; Publication No. US20030219459A1
; GENERAL INFORMATION:
; APPLICANT: Bachmann, Martin
; APPLICANT: Maurer, Patrick
; APPLICANT: Pelliccioli, Erica
; APPLICANT: Renner, Wolfgang A.
; TITLE OF INVENTION: Pion Protein Carrier-Conjugates
; FILE REFERENCE: 1700.0290003
; CURRENT APPLICATION NUMBER: US/10/346,190
; CURRENT FILING DATE: 2003-01-17
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/396,590
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/393,725
; PRIOR FILING DATE: 2002-07-08
; PRIOR APPLICATION NUMBER: 60/389,898
; PRIOR FILING DATE: 2002-06-20
; PRIOR APPLICATION NUMBER: PCT/IB02/00166
; PRIOR FILING DATE: 2002-01-21
; PRIOR APPLICATION NUMBER: 10/050,902
; PRIOR FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 164
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 96
; LENGTH: 131
; TYPE: PRT
; ORGANISM: RNA-phage AP205
US-10-346-190-96

Query Match      98.8%; Score 660; DB 15; Length 131;
Best Local Similarity 99.2%; Pred. No. 7e-70;
Matches 130; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 MANKMPQITSTANKIWSDPTRLSTTFSASLLRQVRKVGVIAELNNVSGQYVSVKRPAP 60
Db      1 MANKTQPISTANKIWSDPTRLSTTFSASLLRQVRKVGVIAELNNVSGQYVSVKRPAP 60

QY      61 KPEGCADACVIMPNENQSIPTVSGSAENLATLKAETHKRNVDTLFASGNAGLGLDLP 120
Db      61 KPEGCADACVIMPNENQSIPTVSGSAENLATLKAETHKRNVDTLFASGNAGLGLDLP 120

QY      121 TAAIVSSDTTA 131
Db      121 TAAIVSSDTTA 131
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Db 121 TAAIVSSDTTA 131

RESULT 15
 US-10-465-811-93
 ; Sequence 93, Application US/10465811
 ; Publication No. US20040005338A1
 ; GENERAL INFORMATION:
 ; APPLICANT: BACHMANN, MARTIN F
 ; APPLICANT: RENNER, WOLFGANG A
 ; TITLE OF INVENTION: PACKAGED VIRUS-LIKE PARTICLES FOR USE AS ADJUVANTS:
 ; FILE OF INVENTION: METHOD OF PREPARATION AND USE
 ; FILE REFERENCE: 1700.0290004
 ; CURRENT APPLICATION NUMBER: US/10/465,811
 ; CURRENT FILING DATE: 2003-06-20
 ; PRIOR APPLICATION NUMBER: US 60/389,898
 ; PRIOR FILING DATE: 2002-06-20
 ; NUMBER OF SEQ ID NOS: 131
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 93
 ; LENGTH: 131
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Bacteriophage AP205 mutant
 US-10-465-811-93

Query Match 98.8%; Score 660; DB 15; Length 131;
 Best Local Similarity 99.2%; Pred. No. 7e-70; Mismatches 0; Indels 0; Gaps 0;
 Matches 130; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MANKPQPISTANKIIVMSDPTRLSTFTSASLLRQVRKVGIAELNNVSGQYVSVYKRPAP 60
 Db 1 MANKTQPISTANKIIVMSDPTRLSTFTSASLLRQVRKVGIAELNNVSGQYVSVYKRPAP 60
 QY 61 KPEGCADACVIMPENQSIPTVIGSAENLATLKAWEETHKRNVDTLFASGNAGLGFLDP 120
 Db 61 KPEGCADACVIMPENQSIPTVIGSAENLATLKAWEETHKRNVDTLFASGNAGLGFLDP 120
 QY 121 TAAIVSSDTTA 131
 Db 121 TAAIVSSDTTA 131

Search completed: June 1, 2005, 09:50:59
 Job time : 92 secs

GenCore version 5.1.6
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QM protein - protein search, using sw model

Run on: June 1, 2005, 09:35:42 ; Search time 30 Seconds
(without alignments)
325.968 Million cell updates/sec

Title: US-10-617-876-1

Perfect score: 668

Sequence: 1 MANKPQPTSTANKIVMSD.....NAGLGFLDPTAIVSSDTTA 131

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Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
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4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
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6: /cgn2_6/ptodata/1/iaa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	79	11.8	332	4	US-09-313-942-10
2	79	11.8	488	2	US-08-599-455B-5
3	79	11.8	488	3	US-09-069-781B-5
4	79	11.8	488	3	US-09-137-132-5
5	79	11.8	488	3	US-08-864-564A-5
6	79	11.8	488	4	US-09-094-410-5
7	79	11.8	488	4	US-08-708-123D-5
8	79	11.8	488	4	US-08-583-153A-5
9	79	11.8	488	4	US-08-638-524B-5
10	79	11.8	658	2	US-08-825-558-4
11	79	11.8	658	3	US-09-312-611-4
12	79	11.8	708	1	US-07-797-556-2
13	79	11.8	708	1	US-08-308-881-2
14	79	11.8	708	2	US-09-058-263-2
15	79	11.8	708	2	US-09-059-099-2
16	79	11.8	708	3	US-09-058-264-2
17	79	11.8	708	4	US-09-455-962-2
18	79	11.8	708	5	PCT-US95-06530-2
19	79	11.8	858	4	US-09-313-942-7
20	79	11.8	918	2	US-08-825-558-6
21	79	11.8	918	3	US-09-312-611-6
22	79	11.8	918	4	US-09-853-180B-3
23	79	11.8	951	4	US-09-313-942-9
24	79	11.8	1158	4	US-09-313-942-26
25	79	11.8	1168	4	US-09-313-942-24
26	73	10.9	488	4	US-09-252-991A-28535
27	72	10.8	185	4	US-09-252-991A-31599

28	70.5	10.6	248	4	US-09-252-991A-20247	Sequence 20247, A
29	70.5	10.6	5087	3	US-09-144-085-1	Sequence 1, Appli
30	70.5	10.6	6095	3	US-09-144-085-2	Sequence 2, Appli
31	70	10.5	179	4	US-09-270-767-43725	Sequence 43725, A
32	70	10.5	520	4	US-09-461-325-144	Sequence 144, App
33	70	10.5	520	4	US-10-012-542-144	Sequence 144, App
34	70	10.5	520	4	US-10-115-123-144	Sequence 144, App
35	69	10.3	414	4	US-09-489-039A-13320	Sequence 13320, A
36	69	10.3	694	4	US-09-328-352-7276	Sequence 7276, A
37	67.5	10.1	300	4	US-09-252-991A-19422	Sequence 19422, A
38	67.5	10.1	343	3	US-08-858-003-32	Sequence 32, Appli
39	67.5	10.1	343	3	US-09-078-166-32	Sequence 32, Appli
40	67.5	10.1	343	3	US-08-997-467-32	Sequence 32, Appli
41	67	10.0	701	4	US-09-538-092-303	Sequence 303, App
42	67	10.0	707	4	US-09-021-560-4	Sequence 4, Appli
43	67	10.0	707	4	US-09-202-178A-4	Sequence 4, Appli
44	66.5	10.0	480	4	US-09-710-279-2852	Sequence 2852, Ap
45	66.5	10.0	480	4	US-09-710-279-2986	Sequence 2986, Ap

ALIGNMENTS

RESULT 1

US-09-313-942-10
; Sequence 10, Application US/09313942
; Patent No. 6472179
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; TITLE OF INVENTION: AND USING
; FILE REFERENCE: REG 203-A
; CURRENT APPLICATION NUMBER: US/09/313,942
; CURRENT FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 09/313,942
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 60/101,858
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 332
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-313-942-10

Query Match 11.8%; Score 79; DB 4; Length 332;
Best Local Similarity 25.5%; Pred. No. 0.36;
Matches 25; Conservative 21; Mismatches 36; Indels 16; Gaps 5;
QY 9 ITSTANKIVMSDPTRLSTTFSASLLR-ORVKVGIAELNNVSGQVSVYKRPAPKPEGCAD 67
Db 82 INRTASSVFTDIFASLNILTCNLTGQLEQNVGITIISG-----LPPEKPKNL-- 132
QY 68 ACVIMENQSTRTVISGSAENLA-----TLKAEWETHK 101
Db 133 SCIV--NEGKORCEWDGGRGTHLETNFTLKSEWATHK 168

RESULT 2

US-08-599-455B-5
; Sequence 5, Application US/08599455B
; Patent No. 5972621
; GENERAL INFORMATION:
; APPLICANT: Tartaglia, Louis A.
; APPLICANT: Tepper, Robert I.
; TITLE OF INVENTION: METHODS OF IDENTIFYING COMPOUNDS THAT
; TITLE OF INVENTION: MODULATE BODY WEIGHT USING THE OB RECEPTOR
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street

```
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/599,455B
; FILING DATE: 22-JAN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/583,153
; FILING DATE: 28-DEC-1995
; APPLICATION NUMBER: 08/570,142
; FILING DATE: 11-DEC-1995
; APPLICATION NUMBER: 08/569,485
; FILING DATE: 08-DEC-1995
; APPLICATION NUMBER: 08/566,622
; FILING DATE: 04-DEC-1995
; APPLICATION NUMBER: 08/562,663
; FILING DATE: 27-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Meiklejohn, Ph.D., Anita L.
; REGISTRATION NUMBER: 35,283
; REFERENCE/DOCKET NUMBER: 07334/017001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 488 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-599-455B-5

Query Match 11.8%; Score 79; DB 2; Length 488;
Best Local Similarity 25.5%; Pred. No. 0.64;
Matches 25; Conservative 21; Mismatches 36; Indels 16; Gaps 5;

Qy 9 ITSTANKIWMSPDTRLSTTFSASLLR-QRVKVGIAELNNVSGQVSVYKRPAPKPECCAD 67
Db 53 INRTASSVTFTDIASLNILQTCNLTGQLEQNVYGIITISG-----LPPEKPKNL-- 103
Qy 68 ACVIMPNENQSIRTVISGSAENLA----TLKAEWETHK 101
Db 104 SCIV--NEGKKMRCWDGGRETHLETNFTLKSEWATHK 139

RESULT 3
US-09-069-781B-5
; Sequence 5, Application US/09069781B
; Patent No. 6287782
; GENERAL INFORMATION:
; APPLICANT: Tartaglia, Louis A.
; APPLICANT: Tepper, Robert I.
; APPLICANT: Culpepper, Janice A.
; APPLICANT: White, David W.
; TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR
; TITLE OF INVENTION: THE DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS,
; TITLE OF INVENTION: INCLUDING OBESITY AND CACHEXIA
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:

; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/599,455B
; FILING DATE: 22-JAN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/583,153
; FILING DATE: 28-DEC-1995
; APPLICATION NUMBER: 08/570,142
; FILING DATE: 11-DEC-1995
; APPLICATION NUMBER: 08/569,485
; FILING DATE: 08-DEC-1995
; APPLICATION NUMBER: 08/566,622
; FILING DATE: 04-DEC-1995
; APPLICATION NUMBER: 08/562,663
; FILING DATE: 27-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Meiklejohn, Ph.D., Anita L.
; REGISTRATION NUMBER: 35,283
; REFERENCE/DOCKET NUMBER: 07334/082001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 488 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-09-069-781B-5

Query Match 11.8%; Score 79; DB 3; Length 488;
Best Local Similarity 25.5%; Pred. No. 0.64;
Matches 25; Conservative 21; Mismatches 36; Indels 16; Gaps 5;

Qy 9 ITSTANKIWMSPDTRLSTTFSASLLR-QRVKVGIAELNNVSGQVSVYKRPAPKPECCAD 67
Db 53 INRTASSVTFTDIASLNILQTCNLTGQLEQNVYGIITISG-----LPPEKPKNL-- 103
Qy 68 ACVIMPNENQSIRTVISGSAENLA----TLKAEWETHK 101
Db 104 SCIV--NEGKKMRCWDGGRETHLETNFTLKSEWATHK 139

RESULT 4
US-09-137-132-5
; Sequence 5, Application US/09137132
; Patent No. 6380363
; GENERAL INFORMATION:
; APPLICANT: Tartaglia, Louis A.
; APPLICANT: Tepper, Robert I.
; APPLICANT: Culpepper, Janice A.
; APPLICANT: White, David W.
; TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR
; TITLE OF INVENTION: THE DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS,
; TITLE OF INVENTION: INCLUDING OBESITY AND CACHEXIA
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
```



```

; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/137,132
; FILING DATE: 18-AUG-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/864,564
; FILING DATE: 28-MAY-1997
; APPLICATION NUMBER: 08/708,123
; FILING DATE: 03-SEP-1996
; APPLICATION NUMBER: 08/638,524
; FILING DATE: 26-APR-1996
; APPLICATION NUMBER: 08/599,455
; FILING DATE: 22-JAN-1996
; APPLICATION NUMBER: 08/583,153
; FILING DATE: 28-DEC-1995
; APPLICATION NUMBER: 08/570,142
; FILING DATE: 11-DEC-1995
; APPLICATION NUMBER: 08/569,485
; FILING DATE: 08-DEC-1995
; APPLICATION NUMBER: 08/566,622
; FILING DATE: 04-DEC-1995
; APPLICATION NUMBER: 08/562,663
; FILING DATE: 27-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Meiklejohn, Ph.D., Anita L.
; REGISTRATION NUMBER: 35,283
; REFERENCE/DOCKET NUMBER: 07334/019004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 488 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-09-137-132--5

Query Match 11.8%; Score 79; DB 3; Length 488;
Best Local Similarity 25.5%; Pred. No. 0.64;
Matches 25; Conservative 21; Mismatches 36; Indels 16; Gaps 5;

QY 9 ITSTANKIVMSDPTRLSTTFSASLLR-ORVKVGIAELNNVSGQVSVYKRPAPKPGCAD 67
Db 53 INRTASSVTFTDIASLNILQTCNLTGQLEQNVYGITIISG-----LPPEKPKNL-- 103

QY 68 ACVIMNENQSIKTVISGSAENLA-----TLKAEWETHK 101
Db 104 SCIV--NEGKQRCWDGGRETHLETNFTLKSEWATHK 139

RESULT 5
US-08-864-564A-5
; Sequence 5, Application US/08864564A
; Patent No. 6395498
; GENERAL INFORMATION:
; APPLICANT: Tartaglia, Louis A.
; APPLICANT: Tepper, Robert I.
; APPLICANT: Cupepper, Janice A.
; APPLICANT: White, David W.
; TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR
; TITLE OF INVENTION: THE DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS,
; TITLE OF INVENTION: INCLUDING OBESITY AND CACHEXIA
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.

```

```

; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/864,564A
; FILING DATE: 28-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/708,123
; FILING DATE: 03-SEP-1996
; APPLICATION NUMBER: 08/638,524
; FILING DATE: 26-APR-1996
; APPLICATION NUMBER: 08/599,455
; FILING DATE: 22-JAN-1996
; APPLICATION NUMBER: 08/583,153
; FILING DATE: 28-DEC-1995
; APPLICATION NUMBER: 08/570,142
; FILING DATE: 11-DEC-1995
; APPLICATION NUMBER: 08/569,485
; FILING DATE: 08-DEC-1995
; APPLICATION NUMBER: 08/566,622
; FILING DATE: 04-DEC-1995
; APPLICATION NUMBER: 08/562,663
; FILING DATE: 27-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Meiklejohn, Ph.D., Anita L.
; REGISTRATION NUMBER: 35,283
; REFERENCE/DOCKET NUMBER: 07334/019002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 488 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-864-564A-5

Query Match 11.8%; Score 79; DB 3; Length 488;
Best Local Similarity 25.5%; Pred. No. 0.64;
Matches 25; Conservative 21; Mismatches 36; Indels 16; Gaps 5;

QY 9 ITSTANKIVMSDPTRLSTTFSASLLR-ORVKVGIAELNNVSGQVSVYKRPAPKPGCAD 67
Db 53 INRTASSVTFTDIASLNILQTCNLTGQLEQNVYGITIISG-----LPPEKPKNL-- 103

QY 68 ACVIMNENQSIKTVISGSAENLA-----TLKAEWETHK 101
Db 104 SCIV--NEGKQRCWDGGRETHLETNFTLKSEWATHK 139

RESULT 6
US-09-094-410-5
; Sequence 5, Application US/09094410
; Patent No. 6403552
; GENERAL INFORMATION:
; APPLICANT: Tartaglia, Louis A.
; APPLICANT: Tepper, Robert I.
; APPLICANT: Cupepper, Janice A.
; APPLICANT: White, David W.
; TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR
; TITLE OF INVENTION: THE DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS,
; TITLE OF INVENTION: INCLUDING OBESITY AND CACHEXIA
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:

```

```

; TITLE OF INVENTION: INCLUDING OBESITY AND CACHEXIA
;
; NUMBER OF SEQUENCES: 50
;
; CORRESPONDENCE ADDRESS:
;
; ADDRESSEE: Fish & Richardson, P.C.
;
; STREET: 225 Franklin Street
;
; CITY: Boston
;
; STATE: MA
;
; COUNTRY: US
;
; ZIP: 02110-2804
;
; COMPUTER READABLE FORM:
;
; MEDIUM TYPE: Diskette
;
; COMPUTER: IBM Compatible
;
; OPERATING SYSTEM: Windows95
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; SOFTWARE: FastSeq for Windows Version 2.0
;
; CURRENT APPLICATION DATA:
;
; APPLICATION NUMBER: US/08/708,123D
;
; FILING DATE: 03-SEP-1996
;
; PRIOR APPLICATION DATA:
;
; APPLICATION NUMBER: 08/638,524
;
; FILING DATE: 26-APR-1996
;
; APPLICATION NUMBER: 08/599,455
;
; FILING DATE: 22-JAN-1996
;
; APPLICATION NUMBER: 08/583,153
;
; FILING DATE: 28-DEC-1995
;
; APPLICATION NUMBER: 08/570,142
;
; FILING DATE: 11-DEC-1995
;
; APPLICATION NUMBER: 08/569,485
;
; FILING DATE: 08-DEC-1995
;
; APPLICATION NUMBER: 08/566,622
;
; FILING DATE: 04-DEC-1995
;
; APPLICATION NUMBER: 08/562,663
;
; FILING DATE: 27-NOV-1995
;
; ATTORNEY/AGENT INFORMATION:
;
; NAME: Meiklejohn, Ph.D., Anita L.
;
; REGISTRATION NUMBER: 35,283
;
; REFERENCE/DOCKET NUMBER: 07334/019001
;
; TELECOMMUNICATION INFORMATION:
;
; TELEPHONE: 617-542-5070
;
; TELEFAX: 617-542-8906
;
; TELEX: 200154
;
; INFORMATION FOR SEQ ID NO: 5:
;
; SEQUENCE CHARACTERISTICS:
;
; LENGTH: 488 amino acids
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; TYPE: amino acid
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; TOPOLOGY: unknown
;
; MOLECULE TYPE: protein
;
; US-08-708-123D-5

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Query Match	11.8%;	Score 79;	DB 4;	Length 488;
Best Local Similarity	25.5%;	Pred. No. 0.64;		
Matches	25;	Conservative 21;	Mismatches 36;	Indels 16; Gaps 5;
QY	9	ITSTANKIWSDPTRLSTFTFSASLLR-QRVKYGIAELNNVSGQVSVYKRPAPKPECCAD	67	
DB	53	INRTASSVTFTDIASLNILQTCNILLTGQLEQNVYGTIIISG-----LPPEKPKNL--	103	
QY	68	ACVIMPNENQSI RTVWISSAENLA-----TLKAEWETHK	101	
DB	104	SCIV--NEGKQRCWDGGRGRTHELTNFTLKSGEAWTH	139	

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RESULT 8
US-08-583-153A-5
US-08-583-5, Application US/08593153A
; Patent No. 6506877
; GENERAL INFORMATION:
; APPLICANT: Tartaglia, Louis A.
; APPLICANT: Tepper, Robert I.
; APPLICANT: Culpepper, Janice A.
; TITLE OF INVENTION: THE OB RECEP
; TITLE OF INVENTION: DIAGNOSIS AND
; TITLE OF INVENTION: OBESITY AND
; NUMBER OF SEQUENCES: 41

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1	TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR THE	
2	3	4
5	TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING	
6	7	8
9	TITLE OF INVENTION: OBESITY AND CACHEXIA	
10	11	12
13	NUMBER OF SEQUENCES: 41	


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; APPLICATION NUMBER: US/08/825,558
; FILING DATE: 19-MAR-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: ESMOND, ROBERT W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 0623.0530001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)371-2600
; TELEFAX: (202)371-2540
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 658 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-825-558-4

Query Match 11.8%; Score 79; DB 2; Length 658;
Best Local Similarity 25.5%; Pred. No. 1;
Matches 25; Conservative 21; Mismatches 36; Indels 16; Gaps 5;

Qy 9 ITSTANKIVMSDPTRLSTTFASLLR-QRVKVGIAELNNVSGQVSVYKRPAPKEGACD 67
Db 82 INRTASSVTFTDIASLNQITCNILTFGQLEQNVYGITISG-----LPPEKPKNL-- 132
Qy 68 ACVIMPNENOSIRTVISGSAENLA-----TLKAEWETHK 101
Db 133 SCIV--NEGKMRCEWDGGRHLETFNFTLKSEWATHK 168

RESULT 11
US-09-312-611-4
; Sequence 4, Application US/09312611
; Patent No. 6380160
; GENERAL INFORMATION:
; APPLICANT: SHARKEY, ANDREW
; APPLICANT: SMITH, STEPHEN K.
; APPLICANT: DELLOW, KIMBERLEY A.
; TITLE OF INVENTION: Gp130 Lacking the Transmembrane Domain
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX
; STREET: 1100 NEW YORK AVENUE
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 17-MAY-1999
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: ESMOND, ROBERT W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 0623.0530002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)371-2600
; TELEFAX: (202)371-2540
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 658 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-312-611-4

Query Match 11.8%; Score 79; DB 3; Length 658;
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Best Local Similarity 25.5%; Pred. No. 1;
Matches 25; Conservative 21; Mismatches 36; Indels 16; Gaps 5;

Qy 9 ITSTANKIVMSDPTRLSTTFASLLR-QRVKVGIAELNNVSGQVSVYKRPAPKEGACD 67
Db 82 INRTASSVTFTDIASLNQITCNILTFGQLEQNVYGITISG-----LPPEKPKNL-- 132
Qy 68 ACVIMPNENOSIRTVISGSAENLA-----TLKAEWETHK 101
Db 133 SCIV--NEGKMRCEWDGGRHLETFNFTLKSEWATHK 168

RESULT 12
US-07-797-556-2
; Sequence 2, Application US/07797556
; Patent No. 5262522
; GENERAL INFORMATION:
; APPLICANT: Gearing, David P.
; TITLE OF INVENTION: Receptor for Oncostatin M and Leukemia
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 19911122
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Seese, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2607
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-587-0430
; TELEFAX: 206-587-0606
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 708 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-797-556-2

Query Match 11.8%; Score 79; DB 1; Length 708;
Best Local Similarity 25.5%; Pred. No. 1.1;
Matches 25; Conservative 21; Mismatches 36; Indels 16; Gaps 5;

Qy 9 ITSTANKIVMSDPTRLSTTFASLLR-QRVKVGIAELNNVSGQVSVYKRPAPKEGACD 67
Db 82 INRTASSVTFTDIASLNQITCNILTFGQLEQNVYGITISG-----LPPEKPKNL-- 132
Qy 68 ACVIMPNENOSIRTVISGSAENLA-----TLKAEWETHK 101
Db 133 SCIV--NEGKMRCEWDGGRHLETFNFTLKSEWATHK 168

RESULT 13
US-08-308-881-2
; Sequence 2, Application US/08308881
; Patent No. 5783672
; GENERAL INFORMATION:
; APPLICANT: Mosley, Bruce
; APPLICANT: Cosman, David J.
; TITLE OF INVENTION: Receptor for Oncostatin M
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; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 708 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-09-059-099-2
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Query Match      11.8%; Score 79; DB 2; Length 708;
Best Local Similarity 25.5%; Pred. No. 1.1;
Matches 25; Conservative 21; Mismatches 36; Indels 16; Gaps 5;
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```
QY 9 ITSTANKIVMSDPTRLSTTFESALLR-QRVKVGIAELNNVSGQYVSVKRPAPKPEGCAD 67
   |||: : :|||: : :|||: : :|||: : :|||: : :|||: : :|||:
Db 82 INETASSVTFTDIASLNIQLTCNLTFGQLEQNVYGTITISG-----LPPEKPKNL-- 132
```

```
QY 68 ACVIMPENOSIRTVISGSAENLA----TLKAETHK 101
   ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 133 SCIV--NEGKKRCEWDGGRETHLETNFTLKSEWATHK 168
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Search completed: June 1, 2005, 09:47:52
Job time : 32 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 1, 2005, 09:31:22; Search time 114 Seconds
(without alignments)
444.435 Million cell updates/sec

Title: US-10-617-876-1
Perfect score: 668
Sequence: 1 MANKPQPTITSTANKIWSDD.....NAGLGFLDPTAIVSSDDTTA 131

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	668	100.0	131	6	ABR56508 AP205 coa
2	668	100.0	131	6	ABU09694 Bacteriop
3	668	100.0	131	6	ABR44611 AP205 coa
4	668	100.0	131	7	ADD24202 Bacteriop
5	668	100.0	131	7	ADJ82145 Protein f
6	668	100.0	131	7	ADK17201 API prote
7	668	100.0	131	8	ADJ36389 Bacteriop
8	668	100.0	131	8	ADI40710 Bacteriop
9	668	100.0	131	8	ADJ67170 Bacteriop
10	668	100.0	131	8	ADK52204 Bacteriop
11	668	100.0	131	8	ADL98301 Bacteriop
12	660	98.8	131	6	ABR56509 AP205 coa
13	660	98.8	131	6	ABU09695 Bacteriop
14	660	98.8	131	6	ABR44612 AP205 coa
15	660	98.8	131	7	ADD24203 Bacteriop
16	660	98.8	131	7	ADJ82146 Protein f
17	660	98.8	131	7	ADK17202 API prote
18	660	98.8	131	8	ADJ36392 Bacteriop
19	660	98.8	131	8	ADI40712 Bacteriop
20	660	98.8	131	8	ADJ67171 Bacteriop
21	660	98.8	131	8	ADK52205 Bacteriop
22	660	98.8	131	8	ADL98305 Mutant Ba
23	80	12.0	194	5	ABU05510 M. tuberc
24	79	11.8	329	2	AAW17859 Rheumatol
25	79	11.8	329	8	ADR14425 Human NF-

ALIGNMENTS

RESULT 1
ABR56508

ID ABR56508 standard; protein; 131 AA.

XX ABR56508;

XX AC

DT 28-JUL-2003 (first entry)

XX XX

DE AP205 coat protein SEQ ID NO:80.

XX XX

KW Antigen presenting cell; APC; immune response; virus like particle; VLP;
KW Cytostatic; virucide; antibacterial; antiparasitic; fungicide;
KW Antiallergic; immunosuppressive; antiaddictive; antinflammatory;
KW Anthyroid; antidiabetic; neuroprotective; nootropic; osteopathic;
KW Antirheumatic; antiarthritic; vaccine; immunisation; infectious disease;
KW Anti-viral protection; tumour; allergy; drug addiction; Crohn's disease;
KW Graft-versus-host disease; Grave's disease; diabetes; multiple sclerosis;
KW Alzheimer's disease; osteoporosis; rheumatoid arthritis;
KW Inflammatory autoimmune disease.

XX OS Synthetic.

XX WO2003024480-A2.

PN PD

XX PD

XX PD

XX PD

XX PD

XX PD

XX PD

XX PD

XX PD

XX PD

XX PD

XX PD

XX PD

XX PD

XX PD

XX PD

XX PD

XX PD

XX PD

XX PD

XX PD

XX PD

XX PD

XX PD

XX PD

XX PD

XX PD

XX PD

XX PD

XX PD

in an animal comprising introducing (C) into the animal; (2) vaccines comprising (C) together with a pharmaceutical diluent, carrier or excipient; (3) immunising or treating an animal comprising administering the vaccine to the animal, or priming or boosting a T cell response in the animal by administering the vaccine; and (4) enhancing anti-viral protection in an animal comprising introducing (C) into the animal. (C) has cytostatic, virucide, antibacterial, antiparasitic, fungicide, antiallergic, immunosuppressive, antiaddictive, antiinflammatory, antithyroid, antidiabetic, neuroprotective, nootropic, osteopathic, antirheumatic and antiarthritic activities. (C) or the vaccines can be used for enhancing an immune response against an antigen or a VLP in an animal, enhancing anti-viral protection in an animal, or immunising or treating tumours and infectious diseases such as viral, bacterial, parasitic or fungal infections. The vaccine compositions are also useful for preventing or treating allergies, drug addiction, graft-versus-host disease, Crohn's disease, Grave's disease, diabetes, multiple sclerosis, Alzheimer's disease, osteoporosis, rheumatoid arthritis, or inflammatory autoimmune disease. ACC69838 to ACC69852 and ABR56401 to ABR56509 represent sequences used in the exemplification of the present invention

XX SQ Sequence 131 AA;

Query Match 100.0%; Score 668; DB 6; Length 131;
Best Local Similarity 100.0%; Pred. No. 3.9e-73;
Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MANKMPQITSTANKIWSDPTRLSTTFSSALLRQVRKVGIAELNNVSGQVSVYKRPAP 60
DB 1 MANKMPQITSTANKIWSDPTRLSTTFSSALLRQVRKVGIAELNNVSGQVSVYKRPAP 60

QY 61 KPEGCADACVIMPNENQSI RTVSGSAENLATLKAETHKRNVDTLFASGNAGLGLDLP 120
DB 61 KPEGCADACVIMPNENQSI RTVSGSAENLATLKAETHKRNVDTLFASGNAGLGLDLP 120

QY 121 TAAIVSSDDTTA 131
DB 121 TAAIVSSDDTTA 131

RESULT 2
ABU09694
ID ABU09694 standard; protein; 131 AA.

XX AC ABU09694;
XX DT 03-JUL-2003 (first entry)
XX DE Bacteriophage AP205 coat protein.
XX KW Bacteriophage AP205; coat protein; hypotensive; cerebroprotective; cardiant; nephrotropic; ophthalmological; immunostimulant; vaccine; angiotensin peptide moiety carrier conjugate; angiotensin peptide; renin-activated angiotensin system; hypertension; stroke; infarction; congestive heart failure; kidney failure; retinal haemorrhage.
XX OS Bacteriophage AP205.
XX PN WO2003031466-A2.
XX PD 17-APR-2003.
XX PF 07-OCT-2002; 2002WO-EP011219.
XX PR 05-OCT-2001; 2001US-0326998P.
XX PR 07-NOV-2001; 2001US-0331045P.
XX PR 18-JAN-2002; 2002US-00050902.
XX PR 21-JAN-2002; 2002WO-IB000166.
XX PR 19-JUL-2002; 2002US-0396637P.
XX PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
XX PA Bachmann M;
XX PI
XX

DR WPI; 2003-430264/40.
XX N-PSDB; ABX95523.
XX New angiotensin peptide moiety carrier conjugate comprising a carrier and an angiotensin peptide moiety, useful for treating or preventing a PT disorder associated with renin-activated angiotensin, e.g. hypertension or infarction.
XX PS Disclosure; Page 96; 97pp; English.
XX CC The invention describes an angiotensin peptide moiety carrier conjugate comprising: (a) a carrier with at least one first attachment site; and (b) at least one angiotensin peptide moiety with at least one second attachment site. The angiotensin peptide conjugate and compositions comprising them are useful for immunising an animal against an angiotensin peptide, and for treating or preventing a physical disorder associated with renin-activated angiotensin system such as hypertension, stroke, infarction, congestive heart failure, kidney failure, and retinal haemorrhage. The conjugate is also useful for inducing immune responses, including producing antibodies. This is the amino acid sequence of a bacteriophage AP205 coat protein used in the preparation of the vaccine conjugates of the invention

XX SQ Sequence 131 AA;

Query Match 100.0%; Score 668; DB 6; Length 131;
Best Local Similarity 100.0%; Pred. No. 3.9e-73;
Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MANKMPQITSTANKIWSDPTRLSTTFSSALLRQVRKVGIAELNNVSGQVSVYKRPAP 60
DB 1 MANKMPQITSTANKIWSDPTRLSTTFSSALLRQVRKVGIAELNNVSGQVSVYKRPAP 60

QY 61 KPEGCADACVIMPNENQSI RTVSGSAENLATLKAETHKRNVDTLFASGNAGLGLDLP 120
DB 61 KPEGCADACVIMPNENQSI RTVSGSAENLATLKAETHKRNVDTLFASGNAGLGLDLP 120

QY 121 TAAIVSSDDTTA 131
DB 121 TAAIVSSDDTTA 131

RESULT 3
ABR44611
ID ABR44611 standard; protein; 131 AA.

XX AC ABR44611;
XX DT 25-JUL-2003 (first entry)
XX DE AP205 coat protein SEQ ID NO:80.
XX KW Immunostimulatory; virus-like particle; bacteriophage; HBV; LCMV; hepatitis B virus; lymphocytic choriomeningitis virus; vaccine; immunostimulant; cytostatic; antiallergic; virucide; antibacterial; immune response; immunisation; allergy; tumour; breast cancer; neuroblastoma; leukaemia; viral disease; influenza; hepatitis; measles; chicken pox; bacterial infection; tuberculosis; pneumonia; syphilis.
XX OS Synthetic.
XX PN WO2003024481-A2.
XX PD 27-MAR-2003.
XX PF 16-SEP-2002; 2002WO-IB004132.
XX PR 14-SEP-2001; 2001US-0318994P.
XX PR 22-APR-2002; 2002US-0374145P.
XX PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
XX PA (MAUR/) MAURER P.
XX PA (TISS/) TISSOT A.

PA (SCHW/) SCHWARZ K.
PA (MEIJ/) MEIJERINK E.
PA (LIPO/) LIPOWSKY G.
PA (PUMP/) PUMPENS P.
PA (CIEL/) CIELENS I.
PA (RENH/) RENHOFA R.
XX
XX
PI Maurer P, Tissot A, Schwarz K, Meijerink E, Lipowsky G;
PI Pumpens P, Cielems I, Renhofs R, Bachmann MF, Storni T;
XX
XX
DR WPI; 2003-354564/33.
XX
XX
PT New compositions comprising immunostimulatory substances packaged into
PT virus-like particles, useful as a vaccine for enhancing an immune
PT response in animals, e.g. for treating or preventing allergies, tumors or
PT viral infections.
XX
XX
PS Disclosure; Page 319; 323pp; English.
XX
XX
CC The present invention describes a composition (C) for enhancing an immune
CC response in an animal. (C) comprises a virus-like particle (VLP), and an
CC immunostimulatory substance. The immunostimulatory substance is bound to
CC the VLP. Also described: (1) enhancing an immune response in an animal by
CC introducing (C) into the animal; (2) producing (C) for enhancing an
CC immune response in an animal; (3) vaccines comprising (C) together with a
CC pharmaceutical diluent, carrier or excipient; and (4) immunising or
CC treating an animal by: (a) administering the vaccine to the animal; (b)
CC priming a T cell response in the animal by administering the vaccine; or
CC (c) boosting a T cell response in the animal by administering the
CC vaccine. (C) has immunostimulant, cytostatic, antiallergic, virucide and
CC antibacterial activities. (1) can be used in vaccines for enhancing an
CC immune response in an animal, particularly a mammal or human.
CC Specifically, (C) is useful for enhancing a B cell response, a T cell
CC response, or a cytotoxic T-lymphocyte (CTL) response. (C) or a vaccine
CC comprising (C) can also be used for immunising or treating an animal,
CC e.g. humans, sheep, horses, cattle, pigs, dogs, cats, rats, birds,
CC reptiles or fish. (C) is particularly useful in prophylactic or
CC therapeutic vaccines against allergies, tumours (e.g. breast cancers,
CC neuroblastoma, or leukaemia), viral diseases (e.g. influenza, hepatitis,
CC measles or chicken pox), or bacterial infections (e.g. tuberculosis,
CC pneumonia or syphilis). ACC69790 to ACC69815 and ABR44502 to ABR44612
CC represent sequences used in the exemplification of the present invention
XX
XX
SQ Sequence 131 AA;
Query Match 100.0%; Score 668; DB 6; Length 131;
Best Local Similarity 100.0%; Pred. No. 3.9e-73;
Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MANKPMQITSTANKIWSDPTRLSTTFSASLLRQVRKVGVIAELNNVSGQYVSVYKRPAP 60
DB 1 MANKPMQITSTANKIWSDPTRLSTTFSASLLRQVRKVGVIAELNNVSGQYVSVYKRPAP 60
QY 61 KPEGCADACVIMPNENQSIIRTVSSAENLATLKAETHKRNVDTLFASGNAGLGLDP 120
DB 61 KPEGCADACVIMPNENQSIIRTVSSAENLATLKAETHKRNVDTLFASGNAGLGLDP 120
QY 121 TAAIVSSDTTA 131
DB 121 TAAIVSSDTTA 131
RESULT 4
ID ADD24202 standard; protein; 131 AA.
XX
AC ADD24202;
XX
XX 15-JAN-2004 (first entry)
XX Bacteriophage AP205 coat protein #1.
DE Bacteriophage AP205 coat protein #1.
XX vaccine composition; virus-like particle; core particle;
KW

KW first attachment site; antigen; antigenic determinant; prion protein;
KW Prp; Prp peptide; vaccine; neuroprotective; antiinflammatory;
KW prion disease; Bovine Spongiform Encephalopathy; BSE;
KW Creutzfeldt-Jakob Disease; prion; AP205; coat protein.
XX
OS Bacteriophage AP205.
XX
PN WO2003059386-A2.
XX
XX 24-JUL-2003.
PD
XX
PF 17-JAN-2003; 2003WO-EP000460.
XX
XX 18-JAN-2002; 2002US-00050902.
PR 21-JAN-2002; 2002WO-IB000166.
PR 08-JUL-2002; 2002US-0393725P.
PR 18-JUL-2002; 2002US-0396590P.
XX
XX (CYTO-) CYTOS BIOTECHNOLOGY AG.
PA
XX Bachmann M, Maurer P, Pelliccioli E, Renner WA;
XX WPI; 2003-598483/56.
DR N-PSDB; ADD24201.
XX
XX A vaccine composition for preventing or treating prion diseases (e.g.
PT Creutzfeldt-Jakob Disease) comprises a virus-like particle (e.g. RNA-
PT phase) and at least one prion protein or peptide bound to the virus-like
PT particle.
XX
XX Disclosure; SEQ ID NO 95; 246pp; English.
XX
XX This invention relates to a novel vaccine composition comprising a virus-
CC like or a core particle with at least one first attachment site and at
CC least one antigen or antigenic determinant that is a prion protein (Prp)
CC or its dimer, or a Prp peptide, the antigen or antigenic determinant
CC being bound to the virus-like or core particle. The vaccine of the
CC invention may have neuroprotective or antiinflammatory activity. The
CC composition is useful as a medicament or in manufacturing a medicament
CC for the treatment or prevention of prion diseases. The prion diseases may
CC include Bovine Spongiform Encephalopathy (BSE) or Creutzfeldt-Jakob
CC Disease. The present sequence is that of a RNA-phase AP205 coat protein
CC which is related to the invention.
XX
SQ Sequence 131 AA;
Query Match 100.0%; Score 668; DB 7; Length 131;
Best Local Similarity 100.0%; Pred. No. 3.9e-73;
Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MANKPMQITSTANKIWSDPTRLSTTFSASLLRQVRKVGVIAELNNVSGQYVSVYKRPAP 60
DB 1 MANKPMQITSTANKIWSDPTRLSTTFSASLLRQVRKVGVIAELNNVSGQYVSVYKRPAP 60
QY 61 KPEGCADACVIMPNENQSIIRTVSSAENLATLKAETHKRNVDTLFASGNAGLGLDP 120
DB 61 KPEGCADACVIMPNENQSIIRTVSSAENLATLKAETHKRNVDTLFASGNAGLGLDP 120
QY 121 TAAIVSSDTTA 131
DB 121 TAAIVSSDTTA 131
RESULT 5
ID ADJ82145 standard; protein; 131 AA.
XX
AC ADJ82145;
XX
XX 06-MAY-2004 (first entry)
XX Protein for RANKL antigen array to treat bone disease.
DE
XX

KW osteopathic; vaccine; core particle; antigenic determinant; RANKL;
 KW bone disease; encephalopathy; immune system stimulation.
 XX Unidentified.
 XX WO2003039225-A2.
 XX 15-MAY-2003.
 XX 07-NOV-2002; 2002WO-EP012449.
 XX 07-NOV-2001; 2001US-0331045P.
 PR 18-JAN-2002; 2002US-00050902.
 PR 21-JAN-2002; 2002WO-IB000166.
 PR 19-JUL-2002; 2002US-0396635P.
 XX (CYTO-) CYTOS BIOTECHNOLOGY AG.
 XX Bachmann M, Maurer P, Spohn G;
 XX WPI; 2003-441430/41.
 XX New compositions comprising a core particle and at least one antigen or
 PT antigenic determinant, useful for as a vaccine for therapy or prophylaxis
 PT of bone diseases, particularly mammalian encephalopathies.
 XX Disclosure; SEQ ID NO 112; 222pp; English.
 XX The invention relates to a composition comprising a core particle having
 CC at least one first attachment site, and at least one antigen or antigenic
 CC determinant having at least one second attachment site. The antigen or
 CC antigenic determinant is a RANKL protein, RANKL fragment or RANKL
 CC peptide. The second attachment site is (non-) naturally occurring with
 CC the antigen or antigenic determinant, and is capable of association to
 CC the first attachment site. The antigen or antigenic determinant and the
 CC core particle interact through the association to form an ordered and
 CC repetitive antigen array. The composition is useful as a medicament, or
 CC for the manufacture of a medicament for treating bone diseases. The
 CC composition is especially useful for as a vaccine for therapy or
 CC prophylaxis of bone diseases, particularly mammalian encephalopathies,
 CC and for stimulating mammalian immune system. This sequence represents a
 CC protein of the invention.
 XX Sequence 131 AA;

Query Match 100.0%; Score 668; DB 7; Length 131;
 Best Local Similarity 100.0%; Pred. No. 3.9e-73;
 Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MANKPMQPTSTANKIIVSDPTRLSTTFSSASLLRQVRKVGVIAELNNVSGQYVSVYKRPAP 60
 Db 1 MANKPMQPTSTANKIIVSDPTRLSTTFSSASLLRQVRKVGVIAELNNVSGQYVSVYKRPAP 60
 QY 61 KPEGCADACVIMPNENQSIKRTVSSAENLATLKAETHKRNVDITLFAAGNAGLGLDLP 120
 Db 61 KPEGCADACVIMPNENQSIKRTVSSAENLATLKAETHKRNVDITLFAAGNAGLGLDLP 120
 QY 121 TAAIVSSDTTA 131
 Db 121 TAAIVSSDTTA 131

RESULT 6
 ADK17201
 ID ADK17201 standard; protein; 131 AA.
 XX AC ADK17201;
 XX DT 06-MAY-2004 (first entry)
 XX AP1 protein for repetitive antigen array.
 XX antiallergic; antiasthmatic; cytostatic; vaccine; virus-like particle;

KW interleukin; IL-5; IL-13; eotaxin; repetitive antigen array;
 KW allergic eosinophilic disease; asthma; Hodgkin's lymphoma.
 XX Unidentified.
 XX WO2003040164-A2.
 XX 15-MAY-2003.
 XX 07-NOV-2002; 2002WO-EP012455.
 XX 07-NOV-2001; 2001US-0331045P.
 PR 18-JAN-2002; 2002US-00050902.
 PR 21-JAN-2002; 2002WO-IB000166.
 PR 19-JUL-2002; 2002US-0396636P.
 XX (CYTO-) CYTOS BIOTECHNOLOGY AG.
 XX Bachmann M, Jennings G, Sonderegger I;
 XX WPI; 2003-441518/41.
 XX Composition comprising an ordered and repetitive antigen or antigenic
 PT determinant array, useful as a medicament, or for manufacturing a
 PT medicament for treating allergic eosinophilic diseases, e.g. asthma, or
 PT Hodgkin's lymphoma.
 XX Disclosure; SEQ ID NO 80; 245pp; English.
 XX The invention relates to a composition comprising a virus-like particle
 CC and at least one antigen, which is a protein or peptide of interleukin
 CC (IL)-5, IL-13 or eotaxin and is bound to the virus-like particle, or a
 CC core particle with at least one first attachment site and at least one
 CC antigen with at least one second attachment site, where the antigen is a
 CC protein or peptide of IL-5, IL-13 or eotaxin. The second attachment site
 CC is an attachment site naturally or not naturally occurring with the
 CC antigen or antigenic determinant. The second attachment site is capable
 CC of association to the first attachment site, and where the antigen or
 CC antigenic determinant and the core particle interact through the
 CC association to form an ordered and repetitive antigen array. The
 CC compositions are useful as medicaments, or for manufacturing a medicament
 CC or a vaccine for treating allergic eosinophilic diseases, e.g. asthma, or
 CC Hodgkin's lymphoma and related diseases. This sequence is used to
 CC generate the compound of the invention.
 XX Sequence 131 AA;

Query Match 100.0%; Score 668; DB 7; Length 131;
 Best Local Similarity 100.0%; Pred. No. 3.9e-73;
 Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MANKPMQPTSTANKIIVSDPTRLSTTFSSASLLRQVRKVGVIAELNNVSGQYVSVYKRPAP 60
 Db 1 MANKPMQPTSTANKIIVSDPTRLSTTFSSASLLRQVRKVGVIAELNNVSGQYVSVYKRPAP 60
 QY 61 KPEGCADACVIMPNENQSIKRTVSSAENLATLKAETHKRNVDITLFAAGNAGLGLDLP 120
 Db 61 KPEGCADACVIMPNENQSIKRTVSSAENLATLKAETHKRNVDITLFAAGNAGLGLDLP 120
 QY 121 TAAIVSSDTTA 131
 Db 121 TAAIVSSDTTA 131

RESULT 7
 ADJ36389
 ID ADJ36389 standard; protein; 131 AA.
 XX AC ADJ36389;
 XX DT 22-APR-2004 (first entry)
 XX Bacteriophage AP205 coat protein virus-like particle.

XX antiallergic; cytostatic; virucide; immunostimulant; vaccine;
 KW immune response; virus-like particle; immunostimulatory; allergy; tumour;
 KW chronic disease; chronic viral disease; bacteriophage AP205;
 KW coat protein; VLP; adjuvant.
 XX Bacteriophage AP205.
 OS
 XX
 XX WO2004000351-A1.
 PN
 XX 31-DEC-2003.
 PD
 XX
 XX 20-JUN-2003; 2003WO-EP006541.
 PF
 XX
 XX 20-JUN-2002; 2002US-0389898P.
 PR
 XX
 XX (CYTO-) CYTOS BIOTECHNOLOGY AG.
 PA
 XX
 XX Bachman MP, Renner WA;
 PI
 XX
 XX WPI; 2004-108361/11.
 DR
 XX
 XX New compositions comprising a virus-like particle (VLP), an
 PT immunostimulatory substance bound to the VLP, and an antigen mixed with
 PT the VLP, useful for enhancing immune response or for treating e.g. tumors
 PT or chronic viral diseases.
 XX
 XX Example 16; SEQ ID NO 90; 252pp; English.
 PS
 XX
 XX The invention describes a composition for enhancing an immune response in
 CC an animal comprising a virus-like particle, an immunostimulatory
 CC substance bound to the virus-like particle, and an antigen mixed with the
 CC virus-like particle. The composition or the vaccine is useful in the
 CC manufacture of a pharmaceutical for the treatment of a disorder or
 CC disease such as allergies, tumours, chronic diseases and chronic viral
 CC diseases. The composition is also useful for enhancing an immune response
 CC in an animal. This is the amino acid sequence of a bacteriophage AP205
 CC coat protein a virus like particle (VLP) that can be used in the adjuvant
 CC of the invention.
 XX
 XX Sequence 131 AA;
 SQ
 Query Match 100.0%; Score 668; DB 8; Length 131;
 Best Local Similarity 100.0%; Pred. No. 3.9e-73;
 Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MANKPQPTITSTANKIWSDPTRLSTTFSSASLLRQKVKGIAELNNVSGQYVSVKRPAP 60
 Db 1 MANKPQPTITSTANKIWSDPTRLSTTFSSASLLRQKVKGIAELNNVSGQYVSVKRPAP 60
 QY 61 KPEGCADACVIMPNENQSI RTVIGSSAENLATLKAETHKRNVDTLFASGNAGLGLDLP 120
 Db 61 KPEGCADACVIMPNENQSI RTVIGSSAENLATLKAETHKRNVDTLFASGNAGLGLDLP 120
 QY 121 TAAIVSSDTTA 131
 Db 121 TAAIVSSDTTA 131
 RESULT 8
 ADI40710
 ID ADI40710 standard; protein; 131 AA.
 XX
 XX ADI40710;
 AC
 XX
 XX 22-APR-2004 (first entry)
 DT
 XX Bacteriophage AP205 coat protein SEQ ID NO:1.
 DE
 XX virus-like particle; bacteriophage AP205; coat protein; cytostatic;
 KW vaccine; gene therapy; cancer; allergy; asthma.
 KW
 XX Bacteriophage AP205.
 OS

XX WO2004007538-A2.
 PN
 XX 22-JAN-2004.
 PD
 XX
 XX 14-JUL-2003; 2003WO-EP007572.
 PF
 XX
 XX 17-JUL-2002; 2002US-0396126P.
 PR
 XX
 XX (CYTO-) CYTOS BIOTECHNOLOGY AG.
 PA
 XX
 XX Bachmann MP, Tissot A, Pumpens P, Cielens I, Renhofa R;
 PI
 XX WPI; 2004-122882/12.
 DR
 XX N-PSDB; ADI40711.
 DR
 XX
 XX New virus-like particle, useful for preparing a composition for treating
 PT or preventing a disease e.g., cancer, allergy or asthma.
 PT
 XX
 XX Claim 1; SEQ ID NO 1; 170pp; English.
 PS
 XX
 XX The present invention describes a virus-like particle (I) which
 CC comprises: (a) a protein having the 131-amino acid sequence of
 CC bacteriophage AP205 coat protein or the mutant coat protein, see ADI40710
 CC or ADI40712 respectively; or (b) a mutein of the protein of (a). Also
 CC described: (1) a mutein of the recombinant protein having the 131-amino
 CC acid sequence; (2) a vector for producing a AP205 virus like particle
 CC comprising a nucleotide sequence being at least 80, 90, 95 or 99%
 CC identical to that of the sequence comprising 3635 or 3613 bp or producing
 CC a recombinant protein comprising a nucleotide sequence encoding a
 CC polypeptide fused to a protein; (3) a pharmaceutical composition
 CC comprising the composition and a carrier; (4) a process for producing a
 CC non-naturally occurring, ordered and repetitive antigen array; (5) a
 CC method of treating or preventing a disease, disorder or physiologic
 CC conditions in an individual; (6) a nucleic acid molecule comprising 3635-
 CC bp sequence; (7) a host cell containing a nucleic acid or a vector; and
 CC (8) a method of producing the virus-like particle. (I) has cytostatic
 CC activity, and can be used in vaccines, and in gene therapy. The virus-
 CC like particle is useful for preparing a composition for treating or
 CC preventing a disease e.g., cancer, allergy or asthma. The present
 CC sequence represents the bacteriophage AP205 coat protein, which is used
 CC in the exemplification of the present invention.
 XX
 XX Sequence 131 AA;
 SQ
 Query Match 100.0%; Score 668; DB 8; Length 131;
 Best Local Similarity 100.0%; Pred. No. 3.9e-73;
 Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MANKPQPTITSTANKIWSDPTRLSTTFSSASLLRQKVKGIAELNNVSGQYVSVKRPAP 60
 Db 1 MANKPQPTITSTANKIWSDPTRLSTTFSSASLLRQKVKGIAELNNVSGQYVSVKRPAP 60
 QY 61 KPEGCADACVIMPNENQSI RTVIGSSAENLATLKAETHKRNVDTLFASGNAGLGLDLP 120
 Db 61 KPEGCADACVIMPNENQSI RTVIGSSAENLATLKAETHKRNVDTLFASGNAGLGLDLP 120
 QY 121 TAAIVSSDTTA 131
 Db 121 TAAIVSSDTTA 131
 RESULT 9
 ADJ67170
 ID ADJ67170 standard; protein; 131 AA.
 XX
 XX ADJ67170;
 AC
 XX
 XX 06-MAY-2004 (first entry)
 DT
 XX Bacteriophage AP205 coat protein for antigen display array.
 DE
 XX anorectic; core particle; antigenic determinant; ghrelin; P-pilin;
 KW

KW antigenic array.
 XX Bacteriophage AP205.
 OS WO2004009124-A2.
 PN 29-JAN-2004.
 XX 18-JUL-2003; 2003WO-EP007849.
 XX 19-JUL-2002; 2002US-0396638P.
 XX (CYTO-) CYTOS BIOTECHNOLOGY AG.
 XX Bachmann MF, Fulurija A;
 PI WPI; 2004-132866/13.
 DR New composition comprising a core particle having a first attachment site
 XX and an antigen or antigenic determinant which is a ghrelin or ghrelin
 XX peptide having a second attachment site, useful for treating obesity.
 PT
 PS Claim 12; SEQ ID NO 28; 175pp; English.
 CC
 CC The invention relates to a new composition comprising: (i) a core
 CC particle with at least one first attachment site; and (ii) at least one
 CC antigen or antigenic determinant with at least one second attachment
 CC site, where the antigen or antigenic determinant is ghrelin or a ghrelin
 CC peptide, and where the second attachment site being consisting of an
 CC attachment site not naturally occurring with the antigen or antigenic
 CC determinant and an attachment site naturally occurring with the antigen
 CC or antigenic determinant, where the second attachment site is capable of
 CC association to the first attachment site, and where the ghrelin or a
 CC ghrelin peptide and the core particle interact through the association to
 CC form an ordered and repetitive antigen array. The composition is useful
 CC for treating obesity. The repetitive array may form part of a phage or
 CC bacterial display array. This peptide corresponds to a Bacteriophage
 CC AP205 coat protein which can be used as part of the repetitive or antigenic
 CC array.
 XX
 SQ Sequence 131 AA;
 Query Match 100.0%; Score 668; DB 8; Length 131;
 Best Local Similarity 100.0%; Pred. No. 3.9e-73;
 Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MANKPMQPIITSTANKIIVMSDPTLSTTFSASLLRQVRKVGIAELNNVSGQYVYKRPAP 60
 Db 1 MANKPMQPIITSTANKIIVMSDPTLSTTFSASLLRQVRKVGIAELNNVSGQYVYKRPAP 60
 Qy 61 KPEGCADACVIMPNENQSIPTVSGSAENLATLKAETHKRNVDTLFASGNAGLGFLDP 120
 Db 61 KPEGCADACVIMPNENQSIPTVSGSAENLATLKAETHKRNVDTLFASGNAGLGFLDP 120
 Qy 121 TAAIVSSDDTTA 131
 Db 121 TAAIVSSDDTTA 131
 RESULT 10
 ADK52204
 ID ADK52204 standard; protein; 131 AA.
 XX
 AC ADK52204;
 XX
 XX 20-MAY-2004 (first entry)
 XX Bacteriophage AP205 coat protein.
 DE
 XX neuroprotective; nootropic; vaccine; amyloid beta 1-6 peptide;
 KW core particle; antigen array; Alzheimer's disease; RNA bacteriophage;
 KW coat protein.
 XX

OS Bacteriophage AP205.
 XX WO2004016282-A1.
 XX 26-FEB-2004.
 XX 18-JUL-2003; 2003WO-EP007864.
 XX 19-JUL-2002; 2002US-0396639P.
 PR 15-MAY-2003; 2003US-0470432P.
 XX (CYTO-) CYTOS BIOTECHNOLOGY AG.
 PA (NOVS) NOVARTIS PHARMA AG.
 XX Bachmann MF, Tissot A, Ortman R, Lueoend R, Staufenbiel M;
 PI Frey P;
 PI WPI; 2004-203731/19.
 DR Composition comprising a core particle with at least one attachment site,
 XX and an antigenic amyloid beta 1-6 peptide, useful for treating diseases
 XX such as Alzheimer's disease.
 PT
 PS Claim 12; SEQ ID NO 28; 184pp; English.
 CC
 CC The invention describes a novel composition comprising a core particle
 CC with at least one attachment site, and an antigenic amyloid beta 1-6
 CC peptide. The new composition comprises: a core particle with at least one
 CC first attachment site; and at least one antigen or antigenic determinant
 CC with at least one second attachment site, where the antigen or antigenic
 CC determinant is a Amyloid beta 1-6 peptide, and where the second
 CC attachment site comprises: an attachment site not naturally occurring
 CC with the antigen or antigenic determinant; or an attachment site
 CC naturally occurring with the antigen or antigenic determinant. The second
 CC attachment site is capable of association to the first attachment site
 CC and the beta 1-6 peptide and the core particle interact through the
 CC association to form an ordered and repetitive antigen array. The
 CC composition is useful for the manufacture of a medicament for treating
 CC Alzheimer's disease and related diseases. This is the amino acid sequence
 CC of an RNA bacteriophage coat protein that can be used in the preparation
 CC of the compositions and vaccines of the invention.
 XX
 SQ Sequence 131 AA;
 Query Match 100.0%; Score 668; DB 8; Length 131;
 Best Local Similarity 100.0%; Pred. No. 3.9e-73;
 Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MANKPMQPIITSTANKIIVMSDPTLSTTFSASLLRQVRKVGIAELNNVSGQYVYKRPAP 60
 Db 1 MANKPMQPIITSTANKIIVMSDPTLSTTFSASLLRQVRKVGIAELNNVSGQYVYKRPAP 60
 Qy 61 KPEGCADACVIMPNENQSIPTVSGSAENLATLKAETHKRNVDTLFASGNAGLGFLDP 120
 Db 61 KPEGCADACVIMPNENQSIPTVSGSAENLATLKAETHKRNVDTLFASGNAGLGFLDP 120
 Qy 121 TAAIVSSDDTTA 131
 Db 121 TAAIVSSDDTTA 131
 RESULT 11
 ADL98301
 ID ADL98301 standard; protein; 131 AA.
 XX
 AC ADL98301;
 XX
 XX 18-NOV-2004 (first entry)
 XX Bacteriophage AP205 coat protein.
 DE
 XX haptan-carrier conjugate; recombinant virus protein; attachment site;
 KW drug addiction; fentanyl; heroin; morphine; amphetamine; cocaine;
 KW

KW methylenedioxymethamphetamine; methamphetamine; methylphenidate;
 KW nicotine; cocaine; nornicotine; PCP; LSD; mescaline; psilocybin;
 KW tetrahydrocannabinol; diazepam; desipramine; imipramine; nortriptyline;
 KW amitriptyline; coat protein.
 XX Bacteriophage AP205.
 XX WO2004009116-A2.
 XX 29-JAN-2004.
 XX 18-JUL-2003; 2003WO-EP007850.
 XX 18-JUL-2002; 2002US-0396575P.
 XX (CYTO-) CYTOS BIOTECHNOLOGY AG.
 XX Bachmann MF, Maurer P;
 XX WPI; 2004-132865/13.
 XX N-PSDB; ADL98302.
 XX Hapten-carrier conjugate useful for treating or preventing addiction to
 PT drug, comprises core particle having first attachment site and hapten
 PT with second attachment site linked to form ordered and repetitive
 PT conjugate.
 XX Claim 14; SEQ ID NO 14; 144pp; English.
 XX The invention comprises a hapten-carrier conjugate consisting of a
 CC carrier (e.g. a recombinant virus protein) that has at least one
 CC attachment site, and at least one hapten with at least one second
 CC attachment site. The method of the invention is useful for treating or
 CC preventing addiction to a drug, such as: codeine, fentanyl, heroin,
 CC morphine, amphetamine, cocaine, methylenedioxymethamphetamine,
 CC methamphetamine, methylphenidate, nicotine, cotinine, nornicotine, PCP,
 CC LSD, mescaline, psilocybin, tetrahydrocannabinol, diazepam, desipramine,
 CC imipramine, nortriptyline and the amitriptyline class of drugs. The
 CC method of the invention is also useful for preventing and treating
 CC diseases associated with addiction. The present amino acid sequence
 CC represents a protein which is claimed for use in the hapten-carrier
 CC conjugate of the invention.
 XX Sequence 131 AA;
 SQ
 Query Match 100.0%; Score 668; DB 8; Length 131;
 Best Local Similarity 100.0%; Pred. No. 3.9e-73;
 Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MANKPMQPISTANKIWSDPTRLSTTFSASLLRQKVKVGI AELNNVSGQYVSVYKRPAP 60
 DB 1 MANKPMQPISTANKIWSDPTRLSTTFSASLLRQKVKVGI AELNNVSGQYVSVYKRPAP 60
 QY 61 KPEGCADACVIMPNENQSI RTVIGSGAENLATLKAETHKRNVDTLFASGNAGLGLDLP 120
 DB 61 KPEGCADACVIMPNENQSI RTVIGSGAENLATLKAETHKRNVDTLFASGNAGLGLDLP 120
 QY 121 TAAIVSSDDTTA 131
 DB 121 TAAIVSSDDTTA 131
 RESULT 12
 ABR56509
 ID ABR56509 standard; protein; 131 AA.
 AC ABR56509;
 XX 28-JUL-2003 (first entry)
 XX AP205 coat protein SEQ ID NO:81.
 DE Antigen presenting cell; APC; immune response; virus like particle; VLP;
 KW

KW cytostatic; virucide; antibacterial; antiparasitic; fungicide;
 KW antiallergic; immunosuppressive; antiaddictive; antinflammatory;
 KW antithyroid; antidiabetic; neuroprotective; nootropic; osteoporosis;
 KW antihemiplegic; antihypertensive; vaccine; immunisation; infectious disease;
 KW anti-viral protection; tumour; allergy; drug addiction; Crohn's disease;
 KW graft-versus-host disease; Grave's disease; diabetes; multiple sclerosis;
 KW Alzheimer's disease; osteoporosis; rheumatoid arthritis;
 KW inflammatory autoimmune disease.
 XX Synthetic.
 XX WO2003024480-A2.
 XX 27-MAR-2003.
 XX 16-SEP-2002; 2002WO-IB004252.
 XX 14-SEP-2001; 2001US-0318967P.
 XX (CYTO-) CYTOS BIOTECHNOLOGY AG.
 XX Bachmann MF, Storni T, Lechner F;
 XX WPI; 2003-363095/34.
 XX A composition, useful for enhancing an immune response against an antigen
 PT or a virus-like particle, enhancing anti-viral protection in an animal,
 PT or immunizing or treating tumors or infectious diseases, e.g. viral
 PT infections.
 XX Disclosure; Page 240-241; 243pp; English.
 XX The present invention describes a composition (C) for enhancing an immune
 CC response against an antigen or a virus-like particle (VLP) bound to at least one antigen, or a
 CC VLP capable of being recognised by the immune system of the animal. Also
 CC described: (1) enhancing an immune response against an antigen or a VLP
 CC in an animal comprising introducing (C) into the animal; (2) vaccines
 CC comprising (C) together with a pharmaceutical diluent, carrier or
 CC excipient; (3) immunising or treating an animal comprising administering
 CC the vaccine to the animal, or priming or boosting a T cell response in
 CC the animal by administering the vaccine; and (4) enhancing anti-viral
 CC protection in an animal comprising introducing (C) into the animal. (C)
 CC has cytostatic, virucide, antibacterial, antiparasitic, fungicide,
 CC antiallergic, immunosuppressive, antiaddictive, antinflammatory,
 CC antihemiplegic, antidiabetic, neuroprotective, nootropic, osteopathic,
 CC antihemiplegic and antihypertensive activities. (C) or the vaccine can be
 CC used for enhancing an immune response against an antigen or a VLP in an
 CC animal, enhancing anti-viral protection in an animal, or immunising or
 CC treating tumors and infectious diseases such as viral, bacterial,
 CC parasitic or fungal infections. The vaccine compositions are also useful
 CC for preventing or treating allergies, drug addiction, graft-versus-host
 CC disease, Crohn's disease, Grave's disease, diabetes, multiple sclerosis,
 CC Alzheimer's disease, osteoporosis, rheumatoid arthritis, or inflammatory
 CC autoimmune disease. ACC69838 to ACC69852 and ABR56401 to ABR56509
 CC represent sequences used in the exemplification of the present invention
 XX Sequence 131 AA;
 SQ
 Query Match 98.8%; Score 660; DB 6; Length 131;
 Best Local Similarity 99.2%; Pred. No. 3.7e-72;
 Matches 130; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MANKPMQPISTANKIWSDPTRLSTTFSASLLRQKVKVGI AELNNVSGQYVSVYKRPAP 60
 DB 1 MANKPMQPISTANKIWSDPTRLSTTFSASLLRQKVKVGI AELNNVSGQYVSVYKRPAP 60
 QY 61 KPEGCADACVIMPNENQSI RTVIGSGAENLATLKAETHKRNVDTLFASGNAGLGLDLP 120
 DB 61 KPEGCADACVIMPNENQSI RTVIGSGAENLATLKAETHKRNVDTLFASGNAGLGLDLP 120
 QY 121 TAAIVSSDDTTA 131
 DB 121 TAAIVSSDDTTA 131

Db	121	TAAIVSSDTTA 131	
RESULT 13			
ABU09695			
ID	ABU09695	standard; protein; 131 AA.	
XX			
AC	ABU09695;		
XX			
DT	03-JUL-2003	(first entry)	
XX			
DE	Bacteriophage AP205	coat protein mutant.	
XX			
KW	Bacteriophage AP205;	coat protein; hypotensive; cerebroprotective;	
KW	cardiant; nephrotoxic; ophthalmological;	immunostimulant; vaccine;	
KW	angiotensin peptide moiety carrier conjugate;	angiotensin peptide;	
KW	renin-activated angiotensin system;	hypertension; stroke; infarction;	
KW	congestive heart failure; kidney failure;	retinal haemorrhage; mutant;	
KW	mutin.		
XX			
OS	Bacteriophage AP205.		
XX			
PH	Key	Location/Qualifiers	
FT	Misc-difference 5	/note= "Wild type Pro substituted by Thr"	
XX			
PN	W02003031466-A2.		
XX			
PD	17-APR-2003.		
XX			
PF	07-OCT-2002;	2002WO-EP011219.	
XX			
PR	05-OCT-2001;	2001US-0326998P.	
PR	07-NOV-2001;	2001US-0331045P.	
PR	18-JAN-2002;	2002US-00050902.	
PR	21-JAN-2002;	2002WO-IB000166.	
PR	19-JUL-2002;	2002US-0396637P.	
XX			
PA	(CYTO-) CYTOS BIOTECHNOLOGY AG.		
XX			
PI	Bachmann M;		
XX			
DR	WPI; 2003-430264/40.		
DR	N-PSDB; ABX95524.		
XX			
PT	New angiotensin peptide moiety carrier conjugate comprising a carrier and		
PT	an angiotensin peptide moiety, useful for treating or preventing a		
PT	disorder associated with renin-activated angiotensin, e.g. hypertension		
PT	or infarction.		
XX			
PS	Disclosure; Page 96; 97pp; English.		
XX			
CC	The invention describes an angiotensin peptide moiety carrier conjugate		
CC	comprising: (a) a carrier with at least one first attachment site; and		
CC	(b) at least one angiotensin peptide moiety with at least one second		
CC	attachment site. The angiotensin peptide moiety conjugate and compositions		
CC	comprising them are useful for immunising an animal against an		
CC	angiotensin peptide, and for treating or preventing a physical disorder		
CC	associated with renin-activated angiotensin system such as hypertension,		
CC	stroke, infarction, congestive heart failure, kidney failure, and retinal		
CC	haemorrhage. The conjugate is also useful for inducing immune responses,		
CC	including producing antibodies. This is the amino acid sequence of a		
CC	bacteriophage AP205 coat protein mutant based on the wild type sequence		
CC	shown in ABU09694 and used in the preparation of the vaccine conjugates		
CC	of the invention		
XX			
SQ	Sequence 131 AA;		
Query Match	98.8%;	Score 660;	DB 6; Length 131;
Best Local Similarity	99.2%;	Pred. No. 3.7e-72;	
Matches 130;	Conservative 0;	Mismatches 1;	Indels 0; Gaps 0;
1	MANKPMQPIITSTANKIIVMSDPTLSTTFSALLRQVRKVGLAELNNVSGQVSVYKRPAP	60	

Db	1	MANKPMQPIITSTANKIIVMSDPTLSTTFSALLRQVRKVGLAELNNVSGQVSVYKRPAP	60
QY	61	KPEGCADACVIMPNENQSIIRTVISGSAENLATIKAEWETHKRNVDTLFASGNAGLGFLDP	120
Db	61	KPEGCADACVIMPNENQSIIRTVISGSAENLATIKAEWETHKRNVDTLFASGNAGLGFLDP	120
QY	121	TAAIVSSDTTA 131	
Db	121	TAAIVSSDTTA 131	
RESULT 14			
ABR44612			
ID	ABR44612	standard; protein; 131 AA.	
XX			
AC	ABR44612;		
XX			
DT	25-JUL-2003	(first entry)	
XX			
DE	AP205	coat protein SEQ ID NO:81.	
XX			
KW	Immunostimulatory; virus-like particle; bacteriophage; HBV; LCMV;		
KW	hepatitis B virus; lymphocytic choriomeningitis virus; vaccine;		
KW	immunostimulant; cytostatic; antiallergic; virucide; antibacterial;		
KW	immune response; immunisation; allergy; tumour; breast cancer;		
KW	neuroblastoma; leukaemia; viral disease; influenza; hepatitis; measles;		
KW	chicken pox; bacterial infection; tuberculosis; pneumonia; syphilis.		
XX			
OS	Synthetic.		
XX			
PN	W02003024481-A2.		
XX			
PD	27-MAR-2003.		
XX			
PF	16-SEP-2002;	2002WO-IB004132.	
XX			
PR	14-SEP-2001;	2001US-0318994P.	
PR	22-APR-2002;	2002US-0374145P.	
XX			
PA	(CYTO-) CYTOS BIOTECHNOLOGY AG.		
PA	(MAUR/) MAURER P.		
PA	(TISS/) TISSOT A.		
PA	(SCHW/) SCHWARZ K.		
PA	(MEIJ/) MEIJERINK E.		
PA	(LIPO/) LIPOWSKI G.		
PA	(PUMP/) PUMPENS P.		
PA	(CIEL/) CIELENS I.		
PA	(RENH/) RENHOFA R.		
XX			
PI	Maurer P, Tissot A, Schwarz K, Meijerink E, Lipowsky G;		
PI	Pumpens P, Cielesns I, Renhofa R, Bachmann MF, Storni T;		
XX			
DR	WPI; 2003-354564/33.		
XX			
PT	New compositions comprising immunostimulatory substances packaged into		
PT	virus-like particles, useful as a vaccine for enhancing an immune		
PT	response in animals, e.g. for treating or preventing allergies, tumors or		
XX	viral infections.		
PS	Disclosure; Page 319-320; 322pp; English.		
XX			
CC	The present invention describes a composition (C) for enhancing an immune		
CC	response in an animal. (C) comprises a virus-like particle (VLP), and an		
CC	immunostimulatory substance. The immunostimulatory substance is bound to		
CC	the VLP. Also described: (1) enhancing an immune response in an animal by		
CC	introducing (C) into the animal; (2) producing (C) for enhancing an		
CC	immune response in an animal; (3) vaccines comprising (C) together with a		
CC	pharmaceutical diluent, carrier or excipient; and (4) immunising or		
CC	treating an animal by: (a) administering the vaccine to the animal; (b)		
CC	priming a T cell response in the animal by administering the vaccine; or		
CC	(c) boosting a T cell response in the animal by administering the		
CC	vaccine. (C) has immunostimulant, cytostatic, antiallergic, virucide and		

CC antibacterial activities. (I) can be used in vaccines for enhancing an
 CC immune response in an animal, particularly a mammal or human.
 CC Specifically, (C) is useful for enhancing a B cell response, a T cell
 CC response, or a cytotoxic T-lymphocyte (CTL) response. (C) or a vaccine
 CC comprising (C) can also be used for immunising or treating an animal,
 CC e.g. humans, sheep, horses, cattle, pigs, dogs, cats, rats, birds,
 CC reptiles or fish. (C) is particularly useful in prophylactic or
 CC therapeutic vaccines against allergies, tumours (e.g. breast cancers,
 CC neuroblastoma, or leukaemia), viral diseases (e.g. influenza, hepatitis,
 CC measles or chicken pox), or bacterial infections (e.g. tuberculosis,
 CC pneumonia or syphilis). ACC69790 to ACC69815 and ABR44502 to ABR44612
 CC represent sequences used in the exemplification of the present invention
 XX
 XX Sequence 131 AA;

Query Match 98.8%; Score 660; DB 6; Length 131;
 Best Local Similarity 99.2%; Pred. No. 3.7e-72;
 Matches 130; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MANKPMQPTITSTANKIWSDPTRLSTTFSASLLRQKVGVIAELNNVSGQVSVYKRPAP 60
 DB 1 MANKTMQPTITSTANKIWSDPTRLSTTFSASLLRQKVGVIAELNNVSGQVSVYKRPAP 60
 QY 61 KPEGCCADACVIMPNENQSI RTVIGSGAENLATLKAETHKRNVDTLFASGNAGLGLDLP 120
 DB 61 KPEGCCADACVIMPNENQSI RTVIGSGAENLATLKAETHKRNVDTLFASGNAGLGLDLP 120
 QY 121 TAAIVSSDTTA 131
 DB 121 TAAIVSSDTTA 131

RESULT 15
 ADD24203
 ID ADD24203 standard; protein; 131 AA.

AC ADD24203;
 DT 15-JAN-2004 (first entry)
 DE Bacteriophage AP205 coat protein #2.
 KW vaccine composition; virus-like particle; core particle;
 KW first attachment site; antigen; antigenic determinant; prion protein;
 KW PrP; PrP peptide; vaccine; neuroprotective; antiinflammatory;
 KW prion disease; Bovine Spongiform Encephalopathy; BSE;
 KW Creutzfeldt-Jakob Disease; prion; AP205; coat protein.
 OS Synthetic.
 OS Bacteriophage AP205.
 PN WO2003059386-A2.
 XX 24-JUL-2003.
 PF 17-JAN-2003; 2003WO-EP000460.
 XX 18-JAN-2002; 2002US-00050902.
 PR 21-JAN-2002; 2002WO-IB000166.
 PR 08-JUL-2002; 2002US-0393725P.
 PR 18-JUL-2002; 2002US-0396590P.
 XX (CYTO-) CYTOS BIOTECHNOLOGY AG.
 XX Bachmann M, Maurer P, Pelliccioli E, Renner WA;
 XX WPI; 2003-598483/56.
 DR N-PSDB; ADD24204.
 XX A vaccine composition for preventing or treating prion diseases (e.g.
 PT Creutzfeldt-Jakob Disease) comprises a virus-like particle (e.g. RNA-
 PT phage) and at least one prion protein or peptide bound to the virus-like
 PT particle.

XX Disclosure; SEQ ID NO 96; 246pp; English.
 XX This invention relates to a novel vaccine composition comprising a virus-
 CC like or a core particle with at least one first attachment site and at
 CC least one antigen or antigenic determinant that is a prion protein (PrP)
 CC or its dimer, or a PrP peptide, the antigen or antigenic determinant
 CC being bound to the virus-like or core particle. The vaccine of the
 CC invention may have neuroprotective or antiinflammatory activity. The
 CC composition is useful as a medicament or in manufacturing a medicament
 CC for the treatment or prevention of prion diseases. The prion diseases may
 CC include Bovine Spongiform Encephalopathy (BSE) or Creutzfeldt-Jakob
 CC Disease. The present sequence is that of a mutant RNA-phase AP205 coat
 XX protein which is related to the invention.

XX Sequence 131 AA;
 Query Match 98.8%; Score 660; DB 7; Length 131;
 Best Local Similarity 99.2%; Pred. No. 3.7e-72;
 Matches 130; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MANKPMQPTITSTANKIWSDPTRLSTTFSASLLRQKVGVIAELNNVSGQVSVYKRPAP 60
 DB 1 MANKTMQPTITSTANKIWSDPTRLSTTFSASLLRQKVGVIAELNNVSGQVSVYKRPAP 60
 QY 61 KPEGCCADACVIMPNENQSI RTVIGSGAENLATLKAETHKRNVDTLFASGNAGLGLDLP 120
 DB 61 KPEGCCADACVIMPNENQSI RTVIGSGAENLATLKAETHKRNVDTLFASGNAGLGLDLP 120
 QY 121 TAAIVSSDTTA 131
 DB 121 TAAIVSSDTTA 131

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